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(54) Title: PLANT STRESS REGULATED GENES

(57) Abstract: The present invention relates to a method to isolate plant genes or gene fragments that are regulated by stress, preferably oxidative stress in plants. The method comprises isolation of plant material, adaptation of the plant material to stress, differential expression of genes or gene fragments in adapted and non-adapted plant material, and isolation of the differential expressed genes or gene fragments. The invention further relates to the genes or gene fragments that can be obtained by this method and to the use of these genes or gene fragments to modulate plant stress tolerance.

PLANT STRESS REGULATED GENES

The present invention relates to a method to isolate plant genes or gene fragments that are regulated by stress, preferably oxidative stress in plants. The method comprises isolation of plant material, adaptation of the plant material to stress, differential expression of genes or gene fragments in adapted and non-adapted plant material, and isolation of the differentially expressed genes or gene fragments. The invention further relates to the genes or gene fragments that can be obtained by this method and to the use of these genes or gene fragments to modulate plant stress tolerance.

Plant molecular responses to environmental stresses are generally very complex and often result in alteration of gene and protein expression as well as in changes in metabolic profiles (Sandermann *et al.*, 1998; Jansen *et al*, 1998; Somssich and Hahlbrock, 1998; Bartels *et al.*, 1996). At least some of those stress responses are required for enhanced stress tolerance as the moderate doses of many stresses increase plant resistance to deleterious stress conditions. For example, raising the temperatures slowly to high, non-lethal temperatures allows plants to tolerate temperatures that are normally lethal, a phenomenon referred to as acclimation (Vierling, 1991). Similarly, exposing maize plants to 14°C acclimates them to lower temperatures that would normally cause chilling injuries (Prasad *et al.* 1994). Also pathogen infection often leads to resistance against subsequent challenges by the same or even unrelated pathogen (reviewed in Sticher *et al.*, 1997). This phenomenon of induced stress tolerance is not restricted to the same kind of the stress and cross-tolerance induced by different kind of stresses has been reported (Örvar *et al.*, 1997; Orzech and Burke, 1988; Keller and Steffen, 1995; Cloutier and Andrews, 1984).

Much of the damage due to environmental constrains has been attributed to the excess production of active oxygen species (AOS), so called oxidative stress (reviewed in Inzé and Van Montagu, 1995). Plant cells acclimated to heat and cold as well as plants expressing systemic acquired resistance to pathogens show also enhanced capacity to tolerate oxidative stress (Banzet *et al.*, 1998, Seppänen *et al.*, 1998, Strobel and Kuc, 1995). This suggests that induced tolerance to oxidative stress is part of the adaptation mechanism to environmental stresses and likely contributes to

the observed phenomenon of cross-tolerance. However, little is known in plants about molecular mechanisms underlying induced tolerance to oxidative stress.

In contrast, adaptive responses to various oxidants have been extensively studied in bacteria and yeast. In both *E. coli* and *S. cerevisiae,* adaptation to oxidative stress is an active process requiring *de novo* protein synthesis (Davies *et al.*, 1995, Storz *et al.*, 1990). At least 80 proteins are induced by adaptive amounts of oxidants in *E. coli*; 40 of them belong to H_2O_2 stimulon and 40 to $O_2^{\bullet-}$ stimulon. Among the induced enzymes are antioxidant enzymes, DNA repair enzyme, heat shock proteins and glucose-6-phosphate dehydrogenase implicated in energy homeostasis (reviewed in Demple, 1991).

Yeast, similarly to bacteria, possess at least two distinct but overlapping adaptive stress responses to oxidants: one induced by H_2O_2 and the other by $O_2^{\bullet-}$ generating compounds (Jamieson, 1992). The H_2O_2 stimulon has been analysed by comparative two-dimensional gel analysis of total cell proteins isolated after treatment with low doses of H_2O_2 (Godon *et al.* 1998). Such a treatment resulted in synthesis of at least 115 proteins and repression of 52 proteins. 70% of those proteins have been identified and classified into cellular processes such as antioxidant defences, heat shock responses and chaperone activities, protein turnover, sulphur, amino acids, purine, and carbohydrate metabolism. Notably, carbohydrate metabolism was redirected to the regeneration of NADPH, which provides reducing power necessary for the detoxification of active oxygen species.

In plants, tolerance to oxidative stress has been previously associated with enhanced activity of antioxidant enzymes and levels of antioxidant metabolites (reviewed in Inzé and Van Montagu, 1995). In addition, Banzet *et al.* (1998) have demonstrated that other stress proteins are likely implicated in acquisition of oxidative stress tolerance by plant cells, similarly as in lower organisms. Expression of small heat shock proteins correlated with adaptation of tomato cells to oxidative stress and additionally, heat shock pre-treatment was able to enhance resistance of those cells to oxidative stress. However, no comparative genome-wide characterisation of induced adaptive responses to oxidative stress has been undertaken in plants.

A genomic approach was used to study the adaptive responses to oxidative stress in leaf tissue of *Nicotiana tabacum.* The redox-cycling compound methyl viologen (MV; paraquat) was used to induce an adaptive response to oxidative stress, as AOS signalling may be important during the defence against both biotic and abiotic stresses

in plants (Levine *et al.*, 1994, Prasad *et al.*, 1994, Banzet *et al.*, 1998, Chamnongpol *et al.*, 1998, Alvarez *et al.*, 1998, Karpinski, 1999). Surprisingly, we found that adaptive amounts of MV enhance the tolerance of tobacco leaf tissues to oxidative stress imposed by toxic levels of the same oxidant. Moreover, adaptation to oxidative stress is associated with induction/repression of approximately 170 genes and partial characterisation of induced genes shows that they are implicated in distinct cellular processes. Several of these defence responses induced by adaptive amounts of oxidants have so far never been associated with the antioxidant response.

It is a first aspect of the invention to provide a method to isolate stress regulated genes or gene fragments, said method comprising

(a) isolating plant material

(b) inducing stress adaptation in said plant material

(c) checking differential expression between stress adapted and non-adapted plant material

(d) isolating differentially expressed genes or gene fragments.

Plant material can be any plant material, such as parts of, or complete, roots, stems or leaves. Plant material may include more than one plant tissue, up to a complete plant. Preferably, said plant is a tobacco plant. Even more preferable, said plant material is leaf material.

Induction of stress adaptation is preferentially carried out by applying sub-lethal stress to said plant material. Stress can be any biotic or abiotic stress, such as fungal or bacterial infection, heat or cold treatment, or oxidative stress. Preferably, said stress is oxidative stress. More preferably, said oxidative stress is applied by putting said plant material in a solution comprising an adequate amount of methyl viologen (methyl viologen pre-treatment). Alternatively, the sub-lethal stress phase may be followed by a period of stronger stress. Said stronger stress may even result in significant cell damage when applied to unadapted plant material.

Differential expression includes induction as well as repression. Checking differential expression can be done with all the differential expression or differential display techniques know to the person skilled in the art, such as, but not limited too, messenger substraction, filter hybridization or micro-array techniques.

Isolation of the differentially expressed genes may be direct or indirect, i.e. by direct isolation of the differentially expressed nucleic acid such as mRNA or cDNA, or by isolation the genes from a library, on the base of the results identifying the gene, such

as filter hybridisation or micro-array. Preferably, the differentially expressed genes or gene fragments are isolated using PCR-based techniques.

A further aspect of the invention is a gene, or gene fragment, obtained by the method according to the invention. A preferred embodiment is a gene or gene fragment, comprising a sequence selected from any of the sequences from SEQ ID N° 1 to SEQ ID N° 167.

Clone names of these sequences, their expression pattern and an indication of the function by homology search is summarized in Table 1.

An even more preferred embodiment is a gene, encoding a protein comprising, preferably essentially consisting, more preferably consisting of SEQ ID N° 169. Preferably, said gene comprises SEQ ID N° 168, more preferably said gene is essentially consisting of SEQ ID N° 168, even more preferably said gene is consisting of SEQ ID N° 168.

Still another aspect of the invention is the use of a gene or a gene fragment according to the invention, or a gene that is at least 60% identical, preferably 80% identical, more preferably 90% identical to said gene or gene fragment according to the invention, or a gene fragment from a gene that is at least 60% identical, preferably 80% identical, more preferably 90% identical to said gene or gene fragment according to the invention to modulate plant stress tolerance. A preferred embodiment is the use of a gene or gene fragment, comprising SEQ ID N° 168, preferably essentially consisting of SEQ ID N° 168, more preferably consisting of SEQ ID N° 168. Preferably, said stress is oxidative stress. Preferably, said plant is tobacco.

A special embodiment is the use of a gene fragment according to the invention, whereby said gene fragment is a promoter. Although the gene fragments isolated by the differential expression procedure may be coding sequences that do not comprise the promoter of the gene, it is obvious for the person skilled in the art to isolate the promoter of a gene when the coding sequence is known. As a non-limiting example, the coding sequence can be used as a probe against a genomic library, whereby the positive scoring clones are subcloned, and the positive subclone is sequenced. On the base of the sequence, the promoter part and the coding part, including the intron – exon boundaries can be predicted using computer software, such as Genemark, Genscan or Grail. Alternatively, the full-length messenger RNA can be isolated, and on the base of its sequence, the start of transcription can be defined, and the promoter can be localized.

Another aspect of the invention is a vector comprising a gene or a gene fragment according to the invention. Said vector may be any vector suitable for eucaryotic cells, as is known to the person skilled in the art, and include but are not limited to self replicating vectors, integrative vectors and virus-based vectors. Preferably, said vector is a plant transformation vector and said eucaryotic cell is a plant cell.

Still another aspect of the invention is a method to modulate stress tolerance in a plant cell or plant, comprising the introduction of the vector according to the invention in said plant cell or plant. Introduction of the vector in the plant cell or plant can be realized by any suitable technique known to the person skilled in the art and includes, but is not limited to transformation techniques such as electroporation, particle bombardment or *Agrobacterium*-mediated transformation, floral dip transformation or sexual techniques such as crossing.

A further aspect of the invention is a plant cell or plant, comprising a vector according to the invention. Preferably, said plant cell or plant is a tobacco plant cell or plant.

DEFINITIONS

Plant material can be any plant tissue such as root, stem or leaf. It may be a part of the plant, such as a disc excised from the leaf, up to the intact plant.

Adaptation as used here means the application of a stress to the plant for a certain time, whereby the time and/or the level of stress are controlled in such a way that the stress applied over the time used is sub-lethal. *Sub-lethal* stress as used here refers to stress that may result in a specific gene expression pattern, but is not leading to cell damage. Detrimental tissue damage can be evaluated by several methods known to the person skilled in the art, but is preferably evaluated by measuring an increase in conductivity as described in the examples. An increase in conductivity in the stress situation, compared with a non-stressed reference situation by less than a factor 5, preferably less than a factor 2, as measured after 42 hours of stress application is considered as non significant.

The term *gene* as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. The term includes double- and single-stranded DNA and RNA. It also includes know types of modifications, for example methylation, “caps” substitution of one or more of the naturally occurring nucleotides with an analogue. It

includes, but is not limited to, the coding sequence. It does include the regulatory sequences such as the promoter and terminator sequences.

Gene fragment may be any gene fragment of at least 40 contiguous nucleotides, preferably 60 nucleotides, more preferably 100 nucleotides, either coding or non-coding. A special case of gene fragment is the promoter of the gene.

Modulation of stress tolerance as used here comprises both the increase of stress tolerance, as well as the decrease of stress tolerance, independent of the level of decrease or increase.

% identical is the percentage identity as measured by a TBLASTN search (Altschull *et al.*, 1997).

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Effect of different concentrations of methyl viologen on leaf discs damage. Three leaf discs were floated on solution with assigned methyl viologen concentrations for indicated time periods. Ion leakage was measured as conductivity of the medium at indicated time intervals. Experiment was done in duplicate and presented value is the average of both measurements. The conductivity of the solution was subtracted from the measured values.

Figure 2. Effect of MV pre-treatment on leaf discs tolerance to 1µM methyl viologen. Leaf discs that were pre-treated for 17 hours with water (grey bars) or 0.1µM methyl viologen (black bars) were exposed to 1µM solution of methyl viologen. Ion leakage was measured as conductivity of the medium in the course of the treatment at regular intervals. The conductivity of the solution was subtracted from measured values. Presented values are average values of nine independent experiments.

Figure 3. Expression of *GPx* and *SodCc* during the treatment with 1µM methyl viologen.

Leaf discs pre-treated with water (0) or 0.1µM MV (0.1) for 17 hours were exposed to 1µM methyl viologen and expression of a glutathione peroxidase gene (*GPx*) and a gene encoding cytosolic CuZnSOD (*SODCc*) was analysed. Total RNA (5 µg) was extracted from 6 leaf discs sampled in two independent experiments at indicated times and subjected to Northern analysis. The same membrane was used for hybridisation

with both genes. Hybridisation of the constitutive actin gene was used as a loading control (bottom panel).

Figure 4. Expression of genes isolated by differential display during the pre-treatment with 0.1µM methyl viologen and the treatment with 1µM methyl viologen.
Total RNA was extracted from 9 leaf discs sampled at indicated times before (c) and during the pre-treatment with 0,1µM MV (0.1) or water (0), and after exposure of pre-treated samples to 1µM MV. Blots with 15µg total RNA each were prepared in quadruplicates and checked for equal loading by methylene blue staining. Each membrane was reused several times.

Figure 5. Resistance to MV of *A. thaliana* transformed with WRKY11 fused to the VP16 activation domain, under control of the 35S promoter. (A) control plate without MV; (B) test plate with 2µM MV. WV9 and WV4: transformed lines, C24: untransformed control.

EXAMPLES

Materials and methods to the examples

Plant Material and Cultivation Conditions.
Nicotiana tabacum cv. Petit Havana SR1 plants were grown in a controlled environment chamber (Weiss technik, Lindenstruth, Germany) under 100 $\mu mol/m^2/s$ light intensity (photosynthetically active radiation), 16h light/ 8h dark regime, relative humidity of 70% and constant temperature of 24°C. The most expanded leaves (11-12 cm long x 7-8 cm wide) from 5 week old plants were used for experiments with methyl viologen.

Methyl Viologen Treatment.
Leaf discs (1cm in diameter) were punched with a cork-bore from the intervenal part of the leaf. Three leaf discs, each originated from different plants, were floated with the abaxial side up on 12 ml of methyl viologen solution in nanopure water or water solely in the case of control. Treatments were performed in controlled environment chambers, under the same conditions as for growth, except otherwise indicated. Leaf

discs for RNA extraction were drained on paper, rapidly frozen in liquid nitrogen and stored at -70°C. Ion leakage from the leaf discs was measured as conductivity of the solution using a conductivity meter (Consort, Turnhout, Belgium).

RNA Extraction and Northern Analysis

Total RNA was extracted from frozen leaf discs using TRIzol™ Reagent (Life Technologies, Paisley, UK) according to the manufacturer's instructions. RNA samples were treated prior to electrophoresis and resolved on 1% agarose gel as described by Shaul *et al.* (1996). The RNA was blotted on nylon membrane (Hybond-N, Amersham International plc., Buckinghamshire, UK or Qiabrane, Qiagen GmbH, Hilden, Germany) by capillary blotting (Maniatis *et al.*, 1982). RNA was fixed to the membrane by crosslinking at 150mJ/cm^2. To check the quality of RNA prior to hybridisation, membranes were incubated for 15 minutes in 5% acetic acid and stained for 5 minutes in 0.04% methylene blue in 0.5 M sodium acetate (pH 5.2), and rinsed with water. After the staining and quality check, membranes were destained in 0.1 x SSC (Maniatis *et al.*, 1982) containing 0.5%SDS (w/v). Membranes were hybridised at 65°C in 50% formamide, 5x SSC, 0.5% SDS and 10% dextran sulphate. ^{32}P-labelled RNA probes corresponding to the cDNA fragments of *GPx* (Criqui *et al.,* 1992), *SodCc*(pSOD3-5'fragment; Tsang *et al.*, 1991), *SodB* (pSOD2-5'fragment; Tsang *et al.* 1991), *Cat1* (pCat1A; Willekens *et al.*, 1994) and *N. tabacum* actin (pRVA12; AventisCropScience, Belgium) were generated by the Riboprobe® System (Promega Corp., Madison, WI, USA). RNA probes corresponding to cDNA fragments isolated by differential display and cloned into pGEM®-T vector (Promega Corp., Madison, WI, USA) were generated according to the same protocol. Membranes were washed at 65°C for 15 minutes each in 3 x SSC (Maniatis *et al.*, 1982), 1 x SSC and 0.1 x SSC (stringent washing) containing 0.5% SDS (w/v). Membranes were exposed to the Storage Phosphor Screen and scanned with the PhosphorImager 445 SI (Molecular Dynamics Inc., Sunnyvale, CA, USA). Membranes were reused after stripping of the probe in 0.1 x SSC at 85°C. Removal of the probe was checked by autoradiography.

Differential display

Total RNA was treated with DNaseI prior to RT-PCR according to the manufacturer's instruction (Life Technologies, Paisley, UK). Alternatively, up to 20 µg of total RNA was incubated with 5U DNaseI, 18U Recombinant Ribonuclease Inhibitor (Promega Corp.,

Madison, WI, USA), 1mM DTT in 80μl of 10mM Tris-Cl, pH8,3, 50mMKCl and 1,5mM $MgCl_2$ for 30 minutes at 37°C. RNA was extracted with phenol/$CHCl_3$ (3:1), ethanol precipitated and dissolved in diethyl pyrocarbonate-treated water. mRNA differential display was performed with the RNA map™ kit (Gene Hunter Corp., Nashville, TN, USA), AmliTaq DNA polymerase (Perkin-Elmer, Branchburg, New Jersey, USA) and [^{33}P] dATP (0,2μl/20μl PCR reaction of 111 000 GBq/mmol; Isotopchim, Ganagobie-Peyruis, France). 3.5 μl of each PCR reaction was mixed with 2μl of loading dye and denatured at 95°C for 5 minutes prior to loading onto 6% DNA sequencing gel. Gels were electrophoresed at 90 Watts constant power until the xylene dye reached the bottom and dried at 80°C for about 1 hour. All the 20 decamers were used in combination with the four T_{12}MN primers provided with the kit. Bands with differential expression pattern and larger than 200 bp were purified from the polyacrylamide gels and reamplified according to the instructions provided in the manual of the RNAmap™ kit. Reamplified cDNA was ethanol precipitated and cloned into pGEM®-T vector (Promega Corp., Madison, WI, USA). Each clone was assigned a number corresponding to the primer used, position on the gel and number of cDNA fragment within the isolated band (e.g. t18-2-5 was amplified with primers T_{12}M<u>T</u> and AP<u>18</u>, isolated as a second from the top of the gel, and after the cloning fifth colony was sequenced).

DNA sequence analysis

3 to 6 cDNAs originating from a single band were sequenced by primer walking using ABI Prism® BigDye™ terminator cycle sequencing kit (PE Applied Biosystems, Foster City, CA, USA). DNA sequence data were analysed using the Wisconsin Package Version 9.1 (Genetics Computer Group (GCG), Madison, Wisc.). The nucleotide sequences of all cloned cDNAs were compared with sequences deposited in GenBank, EMBL, DDBJ, PDB databases, and translated DNA sequences were compared with protein sequences of GenBank CDS translations, PDB, SwissProt, PIR and PRF databases using BLAST algorithm (Altschul *et al.*, 1997). The scoring matrix used by blastp search was BLOSUM62 (Henikoff and Henikoff, 1992). Gene homologues in database were considered to be significant when the e-value was $<10^{-3}$ and the high-scoring segment pair identity was at least 20% for amino acid sequence and 50% for nucleotide sequence.

Plasmid construction

pWRKY11: WRKY11 cDNA amplified from cDNA library with primers EVVRA 28 and EVVRA 29 and cloned in pGEM-t™(Promega) PstI and NotI site via intermediate cloning in the pZErO™ vector (Invitrogen)

pWRKY-pGSJ780A: *Bgl*II-digested *WRKY11* sequence was cloned into the BamHI site of the pGSJ780 binary vector (Bowler et al., 1991).

pWRKY-VP16-pGSJ780A: VP16 activation domain amplified form pTETVP16 by primers EVVRA 26 and EVVRA30 and cloned as Xho1 fragment in Xho1 site of pWRKY11.

The WRKY-VP16 fusion was then cloned as *Bgl*II fragment into the BamHI site of pGSJ780A.

Arabidopsis transformation

Arabidopsis transformation was carried out by the floral dip method (Clouch and Bent, 1998). Selection of primary transgenics and progeny was based on transgene expression levels as determined by Northern blot analysis.

Stress assessment:

80 plants of a F_2-progeny of the transgenic line WV4 (construct pWRKY-VP16-pGSJ780A) were grown on MS+Kanamycine for 2.5 weeks. 15 kanamycine resistant seedlings were transferred to plates containing ½ MS, 1% sucrose and 2 μM methyl viologen (=paraquat) or to ½ MS, 1% sucrose for the controls.

Wild-type *Arabidopsis* plants were treated in a similar way (except for selection on Kanamycine).

Performance of plants was followed and pictures were taken after ~3 weeks.

Example 1: Sensitivity of tobacco to methyl viologen

As a first step in studying adaptive responses to oxidative stress in tobacco, we wanted to establish an experimental system in which low doses of oxidant would induce adaptation to higher doses of the same compound. MV, a redox-active compound that enhances superoxide radical ($O_2^{\bullet-}$) formation mainly in chloroplasts, was used as an oxidant. In order to determine MV concentrations suited for the

induction of adaptation and for the subsequent oxidative stress treatment, sensitivity of tobacco to MV was first determined. Leaf discs were floated on solutions with different concentrations of MV and ion leakage was monitored by measuring the solute conductance. If not scavenged, superoxide generated by MV is converted through redox-reactions into other active oxygen species (AOS) such as hydroxyl radicals that interact with biological molecules and cause oxidative damage (Halliwell and Gutteridge, 1989). Peroxidation of membrane lipids results in loss of membrane integrity that is reflected by enhanced cellular ion leakage. Concentrations lower than 0.2μM MV caused very little increase in ion leakage from the leaf discs in comparison with water-treated controls and no visible damage was seen even after 42 hours of incubation (Figure 1). These concentrations thus seemed most suitable for inducing adaptation to MV. When leaf discs were incubated in MV solutions at concentrations ranging from 0.2–2 μM MV, leaf damage measured as solute conductance clearly correlated with the applied dose of MV. This correlation was more or less linear within this range, suggesting that these doses of MV are most suited for monitoring differences in MV sensitivity between pre-treated and control samples.

Example 2: MV pre-treatment induces tolerance and activates expression of antioxidant genes.

To test, whether exposure to sub-lethal amounts of MV enhances tolerance to higher, normally toxic amounts of this compound, tobacco leaf discs were floated on solutions with less than 0.2 μM MV and subsequently transferred to solutions within the molar range of 0.2-2 μM. Increase in tolerance was assessed by measuring the solute conductance. Leaf discs pre-treated with water were taken as non-adapted controls. Protection against MV was most pronounced (40% in the mean compared to water pre-treated control samples) when leaf discs were pre-treated with 0.1 μM MV for 17 hours (including 8 hours dark period; referred as "pre-treatment") and subsequently treated with 1 μM MV for 11 hours (referred as "treatment")(Figure 2). These parameters for the pre-treatment and the treatment were then used in all further experiments, unless otherwise stated. The specific conditions required for inducing adaptation were not investigated; yet, it was noticed that both the MV concentration and duration of the pre-treatment were factors that affected the level of protection.

mRNA levels of several antioxidant genes were tested by Northern analysis during the pre-treatment and the treatment. Both water and MV caused a rapid induction (1hr) of a glutathione peroxidase gene (*Gpx)* and a gene encoding cytosolic CuZnSOD (*SodCc)* (data not shown). *Gpx* and *SodCc* were only transiently induced in water pre-treated samples, suggesting that this induction was caused by the tissue wounding during leaf discs preparation. In contrast, pre-treatment with 0.1 μM MV gave a persistent increase in *Gpx* and *SodCc* mRNA. After transfer to 1 μM MV, *Gpx* and *SodCc* were again induced in both water and MV pre-treated samples. However, the amount of both messengers remained consistently higher in MV pre-treated samples (Figure 3). The above data indicate that induced tolerance is not just a physiological response but that it involves changes in nuclear gene expression and that GPx and cytosolic CuZnSOD are playing a role in the observed enhanced tolerance of pre-treated samples. *Cat1* and *SodB* genes were also induced following the pre-treatment, but their transcript levels declined during the subsequent treatment with 1μM MV and no correlation could be established between their mRNA levels and enhanced tolerance.

Example 3: Expression of a large number of genes implicated in distinct cellular processes is modulated by MV pre-treatment.

In order to identify which genes other than those encoding antioxidant enzymes would show altered mRNA levels during oxidative stress adaptation, reference samples placed in water for 17 hours, or samples, pre-treated with 0.1 μM MV for 17 hours (adapted leaf discs) were compared by differential mRNA display. To increase the fidelity of the differential display results, mRNA from two independent experiments was used to prepare cDNA, and reverse transcription was performed in duplicates for each RNA sample. Amplified cDNA from two separate experiments and two independent reverse transcription reactions were displayed next to each other on the sequencing gel. Eighty primer combinations yielded 243 bands larger than 150 bp that consistently showed differential expression between adapted and non-adapted samples. 202 of them were up-regulated and 41 were down-regulated. Reamplified cDNA fragments larger than 200bp were cloned and 3 to 6 cDNAs from 60% of all bands sequenced. Sequencing data revealed that 50% of sequenced bands contained two or more cDNA species and 30% of bands were redundant. Taking in account this redundancy and

assuming that only one cDNA species per band contributed to the differential expression pattern, the total number of genes with altered expression after MV pre-treatment is estimated to be 170. Expression of 16 genes was further analysed by Northern analysis with RNA from an independent experiment. The induction of 12 genes was confirmed, while 4 genes remained uninduced. 3 out of these 4 genes were isolated from bands consisting of mixed cDNAs, indicating that they were not responsible for the differential expression pattern. The fact that expression of most of the isolated genes was reconfirmed by Northern analysis is a good indication of procedure fidelity and suggests that the number of genes transcriptionally responding to MV is close to the number estimated by sequencing data.

The nucleotide sequences and translations of 167 cDNAs isolated from differentially expressed bands were compared with non-redundant databases. Only 12 cDNAs were identical or highly similar (>90% over the whole sequence) to previously isolated tobacco genes. Of the other 145 cDNAs, 36 were significantly similar to genes/proteins with known or predicted function, and 16 to genes with no assigned function. The high percentage of cDNAs (62%) for which no similarity was found in the database can in part be attributed to the fact that the isolated cDNAs mostly contain 3`untranslated region where sequence divergence is very high. The homologues of isolated cDNAs, of which the expression was tested and reconfirmed by Northern analysis, are listed in Table 2. Data shows that in addition to antioxidant genes, genes encoding chaperones (*DNAJ*), transporter proteins (*MDR*), dioxygenases (*DIOX*), enzymes of carbohydrate (*ATPC-L*), lipid (*Lox2, MFP*) and terpenoid metabolism (*EAS, VS*), regulatory proteins (*WRKY11, TPK*) and pathogen related proteins (*PRB1b, CBP20*) are activated during MV induced adaptation to oxidative stress in tobacco. The large number as well as the functional diversity of genes transcriptionally responding to MV pre-treatment indicates that AOS activate a wide range of responses within the plant cells.

Example 4: MV induced genes are regulated differently during the treatment.

Of the antioxidant genes tested, only expression of *Gpx* and *SodCc* correlated with enhanced tolerance of pre-treated samples (Figure 3). To further investigate the transcriptional response of genes induced during adaptation to MV, Northern hybridisations were performed for a subset of identified genes (Table 2) during the pre-treatment and the treatment (Figure 4). The earliest gene induction could be observed already after one hour of the pre-treatment for *MFP* and *Lox2* and is likely related to

the wounding of the tissue during the leaf discs preparation. Lipoxygenase (Lox) and multifunctional protein (MFP) are both implicated in a pathway leading to lipid breakdown products such as jasmonic acid, and wounding may induce their expression (Mueller, 1997). This induction was transient and was seen in both water reference samples and MV pre-treated samples.

During the first four hours of the pre-treatment there was no discernible induction of gene expression by MV, while during the treatment, the induction was visible already after three hours. The concentration of MV during the treatment was ten times higher suggesting that the timing of induction is concentration dependent. All genes, except *DIOX*, were induced after 12 hours of the pre-treatment with 0.1μM MV, but more detailed time course analysis would be required to determine exact timing of induction. The low level of induction at this time point reflects probably the preceded dark period of 8 hours with no photosynthetic activity. Primary site of action of MV in photosynthesising plants are the chloroplasts (Halliwell and Gutteridge 1989) and active photosynthesis is required for maximal generation of superoxide by this redox-cycling compound. This is in agreement with the further and much stronger induction of the mRNA level on the light during the last five hours of the pre-treatment.

Expression of all genes, except *DIOX*, was further induced during the treatment with 1μM MV and the induction started within the first three hours of the treatment. In the course of the treatment two different expression patterns were essentially recognised. For one group of genes (*PRB-1b, CBP20, VS, MDR, DNAJ* and *WRKY11*), expression was induced by a 1 μM MV treatment in both, the 0,1 μM MV pre-treated samples and water reference samples as such that the level of transcript remained higher in the 0,1 μM MV pre-treated samples for at least six hours, which is the time when the difference in tolerance between pre-treated and non pre-treated samples began to be manifested. The increase in transcript levels with time was rather slow reaching the maximum between 6-9 hours in water reference samples, while it was generally 3 hours earlier in MV pre-treated samples. Towards the end of the treatment, the transcript level declined. A similar expression pattern was observed for antioxidant genes *GPx* and *SodCc* (Figure 3).

The second group of genes (*EAS, TPK, Lox2* and *MFP*) was also transcriptionally induced by a 1 μM MV treatment (except *Lox2* in MV pre-treated samples) but with different kinetics. The induction was much stronger in the water reference samples, so the differences in mRNA level between MV pre-treaded and the water reference

samples diminished. The response was also faster, with transcript levels reaching a maximum within 3 hours (6 hours for *MFP*) in both, water reference and MV pre-treated samples. The kinetics of *ATPC-L* expression had rather intermediate character with respect to the expression patterns of the two described gene groups. Together these data indicate the presence of at least two different mechanisms for activation of defence genes by MV.

Example 5: overexpression of WRK11 provokes oxidative stress tolerance.

Full-length cDNA sequence was obtained by 5'RACE using total leaf RNA and a gene-specific 3' primer.

The corresponding gene was designated *WRKY11* because 10 non-identical tobacco WRKY genes were already present in the database.

WRKY proteins are divided into 3 classes: based on type and number of WRKY domains. WRKY family members show only little homology among each other outside of the WRKY domains (Eulgem, Rushton et al. 2000). Database search (blastx on nrprot) revealed only 1 protein that is significantly similar to WRKY11 within the N-terminal part of the protein: *St*WRKY1 from potato (Dellagi, Heilbronn et al. 2000).

Segregating populations (F2) of *A. thaliana* plants (C 24) transformed with *WRKY11* under control of the 35S promoter (35S-WRKY11) or with *WRKY 11* fused to the *VP16* activation domain under control of the 35S promoter (35S-WRKY11-VP16) were grown on MS media with kanamycine. ~ 3 weeks old seedlings resistant to kanamycine from 3:1 segregating lines (WV4 and WV9 *WRKY11-VP16* transformed lines) were transferred to the solid media containing ½ MS salts, 1% sucrose and 2 µM methyl viologen (MV) or on plates without MV. As control plants untransformed *A. thaliana* plants were used (C24). After 3-4 weeks, phenotypic differences were assessed.

On control plates without MV, no difference in growth between *WRKY-VP16* transformants and controls were observed (Fig 5 A). On plates containing MV, growth of all plants was retarded, however differences in growth and MV tolerance between lines overexpressing *WRKY11* and control plants were observed.

Line WV4 was more tolerant to MV than untransformed Arabidopsis control (C24). However, line WV9 did not differ significantly from control in its growth and MV tolerance (Fig 5, B).

Table 1: list of stress related genes with identification on the base of homology

Clone number	DD+/-	N+/-/=	h mology E<10-3 with at least 20%amin acids or 50% nucleic acids id ntical
			non-redundant DNA and protein s quenc databases (blastx/blastn)
a1-1-14.seq	+		
a1-1-7.seq	+		
a10-2-12.seq	+		hypothetical protein [Arabidopsis thaliana] (gb|AAD08932)
a10-4-1.seq	+		metallothionein-like protein type 2 Nicotiana plumbaginifolia (gb|U35225)
a10-4-12.seq	+		
a10-4-15.seq	+		
a14-1-1.seq	+	=	serine carboxypeptidase-like protein Oryza sativa (dbj|BAA04511)
a14-1-3.seq	+		
a14-1-4.seq	+		
a18-1-5.seq	+		EREBP-1 Matricaria chamomilla (dbj|BAA87068)
a18-1-8.seq	+		
a18-3-2.seq	+		
a18-3-3.seq	+		EIF-5A (eukaryotic initiation factor 5A2) Solanum tuberosum (sp|P56333)
a18-4-6.seq	+		
a19-3-1.seq	+		
a19-3-3.seq	+		
a19-3-4.seq	+		
a19-3-9.seq	+		
a20-1-3.seq	+		
a3-2-2.seq	-		ribosomal protein L12 (60S) Prunus armeniaca (sp|O50003)
a8-1-1.seq	-		
a8-1-2.seq	-		geranyl-geranyl reductase chlP-gene Nicotiana tabacum (emb|CAA07683)
a8-1-4.seq	-		early wound inducive gene Nicotiana tabacum (dbj|BAA95791)
a9-1-2.seq	+		epoxide hydrolase Nicotiana tabacum (gb|AAB02006)
a9-3-4.seq	+		immediate-early salicylate-induced glucosyltransferase (IS10a) Nicotiana tabacum (gb|U32643)
a9-4-1.seq	+		
a9-5-9.seq	+		
a9-6-11.seq	-		
a9-7-1.seq	+		
a9-7-10.seq	+		lipoxygenase LOX1 Nicotiana tabacum (emb|X84040)
a9-7-11.seq	+		
c1-1-3.seq	+		
c1-1-5.seq	+		
c1-2-2.seq	+		
c1-3-12.seq	-		
c10-3-1.seq	-		
c10-3-5.seq	-		
c11-2-1.seq	+		
c11-3-1.seq	+		
c11-3-3.seq	+		caffeoyl-CoA O-methyltransferase Nicotiana tabacum (emb|Z56282)
c13-1-6.seq	+		
c13-2-1.seq	+		L19 ribosomal protein Nicotiana tabacum (emb|Z31720)
c13-3-13.seq	+		23S 4.5S rRNA genes chlP-genes Nicotiana tabacum (gb|J01446)
c13-3-6.seq	+		
c14-1-60.seq	+		glycolate oxidase Lycopersicon esculentum (pir|T07032)
c14-2-10.seq	+		
c14-2-15.seq	+		ribosomal protein L35-like (60S) Arabidopsis thaliana (emb|CAB85998)
c14-3-4.seq	+		ribosomal protein L23a-like (60S) Arabidopsis thaliana (emb|CAB75762)
c14-5-1.seq	-		predicted protein Oryza sativa (dbj|BAA83350)
c14-6-11.seq	+		predicted protein Arabidopsis thaliana (pir|T02387)
c14-7-4.seq	+		
c15-1-2.seq	+		
c15-1-4.seq	+	+	pathogen- and wound-inducible antifungal protein CBP20 precursor Nicotiana tabacum (gb|AAB29959)
c15-11-2.seq	+		
c15-11-4.seq	+		
c15-2-8.seq	+		hypothetical protein Arabidopsis thaliana (emb|CAB88533)
c15-3-4.seq	+		hypothetical protein Arabidopsis thaliana (gb|AAF63779)
c15-6-2.seq	+		
c15-6-3.seq	+		
c15-7-1.seq	-		
c15-8-5.seq	-		
c17-3-1.seq	+		
c17-3-5.seq	+		

c17-5-5.seq	+		
c17-5-8.seq	-		
c17-6-2.seq	+		
c18-1-2.seq	+	+	DNAJ protein-lik Arabidopsis thaliana (emb|CAB86070)
c18-2-1.seq	+		CCT (chaperonin containing TCP-1) b subunit Oxytricha nova (gb|AF188130)
c19-2-11.seq	+		
c19-3-10.seq	+		
c19-4-19.seq	+		
c19-4-22.seq	+		
c19-5-1.seq	-		
c19-5-4.seq	-		
c19-6-3.seq	+		
c19-7-4.seq	+		putative translation initiation factor 2B beta subunit (NIFb) EIF2B beta homolog Nicotiana tabacum (gb|AF137288)
c2-1-10.seq	-		
c2-11-14.seq	+		
c2-11-2.seq	+		
c2-2-1.seq	+		
c2-2-3.seq	+		
c2-4-1.seq	+		
c2-5-6.seq	+		
c2-6-5.seq	-		
c2-7-1.seq	+		non-sucrose-inducible patatin precursor -strand Solanum brevidens (gb|U09331)
c2-9-14.seq	-		
c20-1-4.seq	+		DNA- binding protein (pabf) Nicotiana tabacum (gb|U06712)
c3-2-4.seq	+		
c3-3-6.seq	+		
c3-4-1.seq	-		
c4-1-2.seq	+		
c4-3-3.seq	+		
c5-1-2.seq	+		
c6-8-13.seq	+		
c6-8-4.seq	+		
c6-8-9.seq	+		
c7-1-2.seq	-		
c7-1-6.seq	-		
c7-3-10.seq	-		
c7-3-3.seq	-		hypothetical protein Arabidopsis thaliana (emb|CAB62623)
c7-3-9.seq	-		
c8-1-5.seq	+		
c9-1-4.seq	+		hypothetical protein Arabidopsis thaliana (dbj|BAB08809)
g10-1-1.seq	+		putative ABA-repsonsive protein Arabidopsis thaliana (dbj|BAB11190)
g12-1-21.seq	-		hypothetical protein Arabidopsis thaliana (pir|T01731)
g12-1-5.seq	-		Putative membrane related protein Arabidopsis thaliana (gb|AAD38248)
g14-2-4.seq	+	+	vetispiradiene synthase Solanum tuberosum (gb|AAD02223)
g14-3-10.seq	+		
g14-3-22.seq	+		hypothetical protein Spinacia oleracea (pir|T09217)
g14-3-3.seq	+		Sequence 162 from Patent EP0953640 Nicotiana tabacum (emb|AX014606)
g14-3-4.seq	+		HR associated Ca2+-binding protein Phaseolus vulgaris (gb|AAD47213)
g14-3-7.seq	+		
g15-1-37.seq	+		putative golgi transport complex protein Arabidopsis thaliana (gb|AAF16568)
g15-2-2.seq	+	=	ubiquitin Nicotiana tabacum (gb|U66264) able to induce HR-like lesions
g15-3-11.seq	-		Sequence 7 from Patent EP0953640 Nicotiana tabacum (emb|AX014451)
g15-3-7.seq	-		
g15-4-1.seq	+		
g17-2-13.seq	+	+	WRKY DNA binding protein Solanum tuberosum (emb|CAB97004)
g17-3-2.seq	+		
g18-4-7.seq	+		putative ribosomal protein L18 (60S) Arabidops thaliana (gb|AAF26138)
g18-5-1.seq	-		
g18-5-12.seq	-		
g18-6-12.seq	+		
g18-6-5.seq	+		
g18-7-5.seq	+		
g18-8-7.seq	+		
g19-1-5.seq	-		unknown protein Arabidopsis thaliana (gb|AAF23197)
g19-1-6.seq	+		
g19-1-7.seq	+		putative protein Arabidopsis thaliana (emb|CAB82697)
g19-2-1.seq	+		
g19-2-9.seq	+		
g2-1-2.seq	+	+	5-epi-aristolochene synthase Nicotiana tabacum(emb|Y08847)
g20-2-20.seq	+		hypothetical protein Arabidopsis thaliana (gb|AAF14679)

g20-2-29.seq	+		
g20-2-31.seq	+		
g3-1-1.seq	+		ankyrin-like protein Arabidopsis thaliana (dbj|BAB10271)
g3-1-4.s q	+	=	ADP-ribosylation factor Capsicum annuum (gb|AAF65512)
g6-2-13.seq	+	+	leucoanthocyanidin dioxyg nase 2, putativ ; 51024-52213 Arabidopsis thaliana (gb|AAG21532)
g6-3-7.s q	+	+	ATP citrate lyase Arabidopsis thaliana (dbj|BAB09916)
g6-4-4.seq	+		
g6-4-5.seq	+		ATP-dependent protease proteolytic subunit ClpP-like protein Arabidopsis thaliana (dbj|BAB09831)
g7-1-1.seq	+		RNA-binding protein MEI2 (meiotic regulator), putative; 36123-32976 Arabidopsis thaliana (gb|AAG12640)
g7-1-4.seq	+		
g9-2-2.seq	+	+	P-glycoprotein-like protein Arabidopsis thaliana (emb|CAB71875)
g9-2-6.seq	+		
g9-3-17.seq	+		
g9-3-4.seq	+		
g9-5-5.seq	+		
g9-6-1.seq	+	+	lipoxygenase Solanum tuberosum (gb|AAD09202)
t12-1-7.seq	+	+	serine/threonine/tyrosine-specific protein kinase APK1A Arabidopsis thaliana (sp|Q06548)
t12-2-1.seq	+		chitinase class 4 Vigna unguiculata (pir|S57476)
t12-2-18.seq	+		
t18-2-5.seq	+	+	basic PRB-1b Nicotiana tabacum (emb|X66942)
t18-3-2.seq	+		
t18-3-6.seq	+		RNA- or ssDNA-binding protein Vicia faba (pir|T12196)
t18-4-18.seq	-		ADP-glucose pyrophosphorylase small subunit Solanum tuberosum (emb|X55650)
t-2-1-1.seq	+		ubiquitin carrier protein Lycopersicon esculentum (sp|P35135)
t2-1-3.seq	+		Hypothetical protein chlP Nicotiana tabacum (sp|P12204)
t2-6-3.seq	+		
t7-1-12.seq	+	=	Hypothetical protein Arabidopsis thaliana (gb|AAF26468)
t7-1-14.seq	+		t7-2-4.seq + intron
t7-2-4.seq	+	+	Multifunctional protein of glyoxysomal fatty acid beta-oxidation Brassica napus (emb|AJ000886)
t7-4-7.seq	+		putative glutathione S-transferase; 80986-80207 Arabidopsis thaliana (gb|AAF15930)
t7-4-8.seq	+		
t7-5-4.seq	+		
t7-5-5.seq	+		
t7-6-4.seq	+		

DD+ = induced on differential display gel
DD- = repressed on differential display gel
N+ = induced on Northern
N- = repressed on Northern
N= = constant on Northern

Table 2. Genes isolated by differential display with induction confirmed by Northern analysis.

Columns refer, respectively to the clone number; the name of the predicted gene, the length of isolated cDNA including both primers; the length of deduced partial protein sequence; the (putative) homologue with highest e-value identified in the database; accession number of a (putative) homologue; percentage of the amino acid sequence identity (superscript indicate homology of the same segment to similar domains localised upstream $^{(1)}$ and downstream $^{(2)}$ in the homologous protein); the length of the high-scoring segment pair(s) identified by blastx homology search.

Clone number	cDNA/ gene name	cDNA length (bp)	Peptide length (aa)	(Putative) homologue	Accession Number	%sequence identity (aa)	HSPS length (aa)
T18-2-5	PRB-1b	448	48	pathogenesis-related protein 1b, PRB-1b (*Nicotiana tabacum*)	emb|X66942	100%	47
C15-1-4	CBP20	508	84	pathogen- and wound-inducible antifungal protein CBP20 (clone *cbp*20-52) (*Nicotiana tabacum*)	gb|AAB29959	98%	84
G2-1-2	EAS	228	8	5-epi-aristolochene synthase (clone *str*319) (*Nicotiana tabacum*)	emb|Y08847	100%	7
G14-2-4	VS	382	66	vetispiradiene synthase (*Solanum tuberosum*)	gb|AAD02223	100%	65
G6-3-7	ATPC-L	397	49	ATP citrate-lyase (*Arabidopsis thaliana*)	dbj|BAB09916	97%	48
C18-1-2	DNAJ	397	89	DnaJ-like protein (*Arabidopsis thaliana*)	emb|CAB86070	75%	88
G9-2-2	MDR	505	96	P-glycoprotein-like protein (*Arabidopsis thaliana*), nucleotide binding fold NBF2	emb|CAB71875	68%[(1)] 91%[(2)]	91 95
G6-2-13	DIOX	525	96	Leucoanthocyanidin dioxygenase 2-like protein (*Arabidopsis thaliana*)	gb|AAG21532	80%	92
G9-6-1	Lox2	269	19	Lipoxygenase (*Solanum tuberosum*)	gb|AAD09202	100%	17
T7-2-4	MFP	413	55	Multifunctional protein of glyoxysomal fatty acid beta-oxidation (*Brassica napus*)	emb|AJ000886	61%	46
T12-1-7	TPK	361	75	Protein tyrosine-serine-threonine kinase APK1A (*Arabidopsis thaliana*)	sp|Q06548	36%	82
G17-2-13	WRKY11	548	87	WRKY DNA binding protein (*Solanum tuberosum*)	emb|CAB97004	94%	86

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CLAIMS

1. A method to isolate stress regulated genes or gene fragments comprising
   (a) isolating plant material
   (b) inducing stress adaptation in said plant material
   (c) checking differential expression between stress adapted and non adapted plant material
   (d) isolating differentially expressed genes or gene fragments.
2. A method according to claim 1, where by said induction of stress adaptation is obtained by a methyl viologen pre-treatment and/or treatment.
3. A method according to claim 1 or 2, whereby said plant material is tobacco leaf material.
4. A method according to any of the claims 1 – 3, whereby said isolation of differentially expressed genes or gene fragments is carried out by PCR reaction.
5. A gene or gene fragment, obtained by a method according to any of the claims 1 – 4.
6. A gene or gene fragment, according to claim 5, comprising a sequence selected from any of the sequences from SEQ ID N°1 to SEQ ID N°167.
7. A gene, according to claim 5, encoding a protein comprising SEQ ID N° 169.
8. A gene according to claim 7, comprising SEQ ID N° 168.
9. The use of a gene according to claim 5, or a gene that is at least 60% identical, preferably 80% identical, more preferably 90% identical to said gene, to modulate plant stress tolerance
10. The use of a gene comprising a sequence selected from any of the sequences from SEQ ID N°1 to SEQ ID N° 167, or a gene that is at least 60% identical, preferably 80% identical, more preferably 90% identical to said gene, to modulate plant stress tolerance.
11. The use of a gene encoding a protein comprising SEQ ID N° 169 to modulate plant stress tolerance.
12. The use of a gene according to claim 11, whereby said gene comprises SEQ ID N° 168.
13. The use of a gene fragment according to claim 5, whereby said gene fragment is a promoter, to modulate plant stress tolerance.

14. The use of a promoter derived from a gene according to claim 5 or 6, or from a gene that is at least 60% identical, preferably 80% identical, more preferably 90% identical to said gene, to modulate plant stress tolerance
15. The use according to claim 9 or 14, whereby said stress is oxidative stress.
16. The use according to any of the claims 9 – 15, whereby said plant is tobacco.
17. A vector comprising a gene or a gene fragment according to any of the claims 5 - 8.
18. A method to modulate stress tolerance of a plant cell or plant, comprising the introduction of a vector according to claim 17 in said plant cell or plant.
19. A plant cell or plant, comprising a vector according to claim 17.

Fig. 1

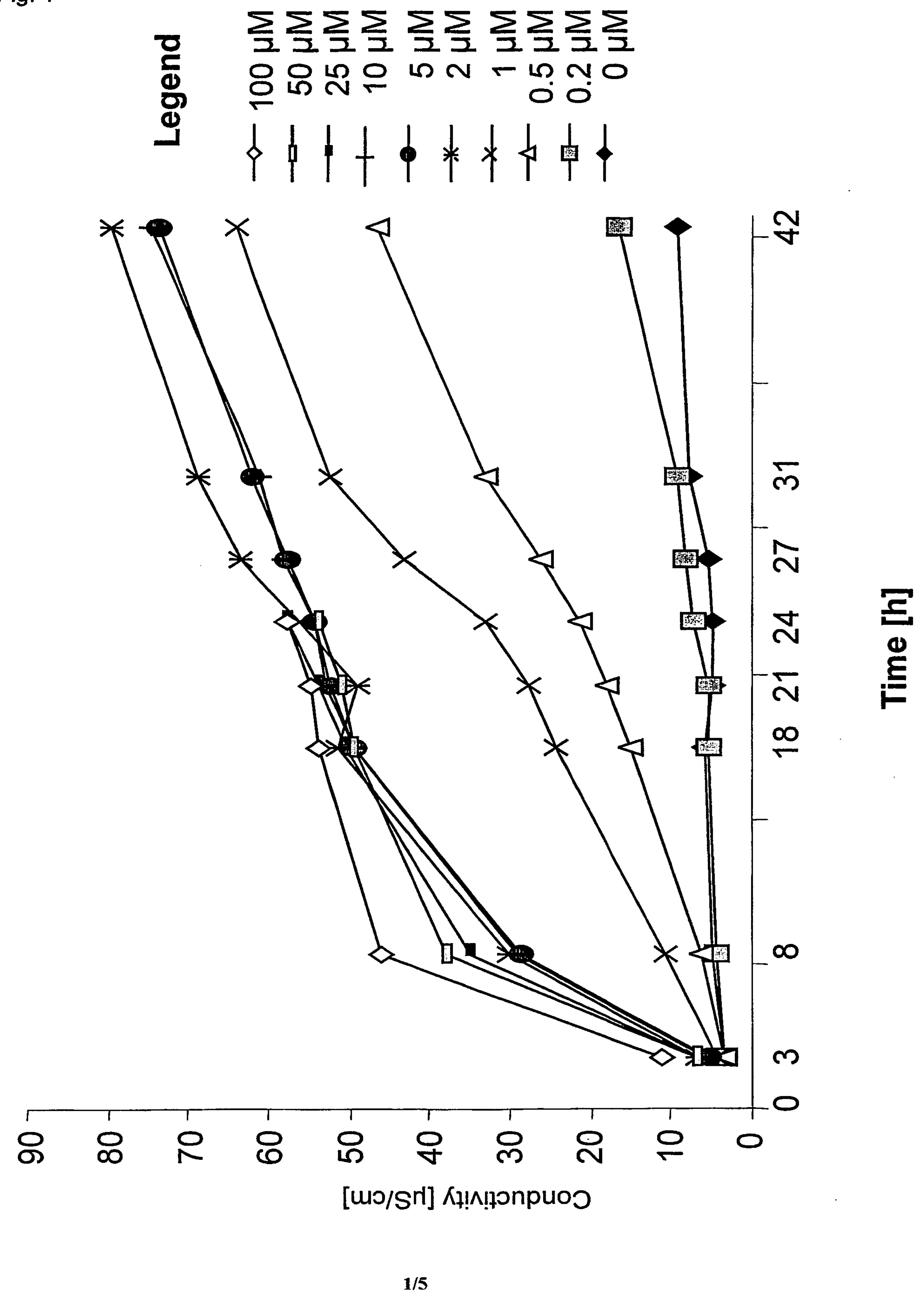

Legend
100 µM
50 µM
25 µM
10 µM
5 µM
2 µM
1 µM
0.5 µM
0.2 µM
0 µM
Conductivity [µS/cm]
0 10 20 30 40 50 60 70 80 90
Time [h]
0 3 8 18 21 24 27 31 42

Fig. 2

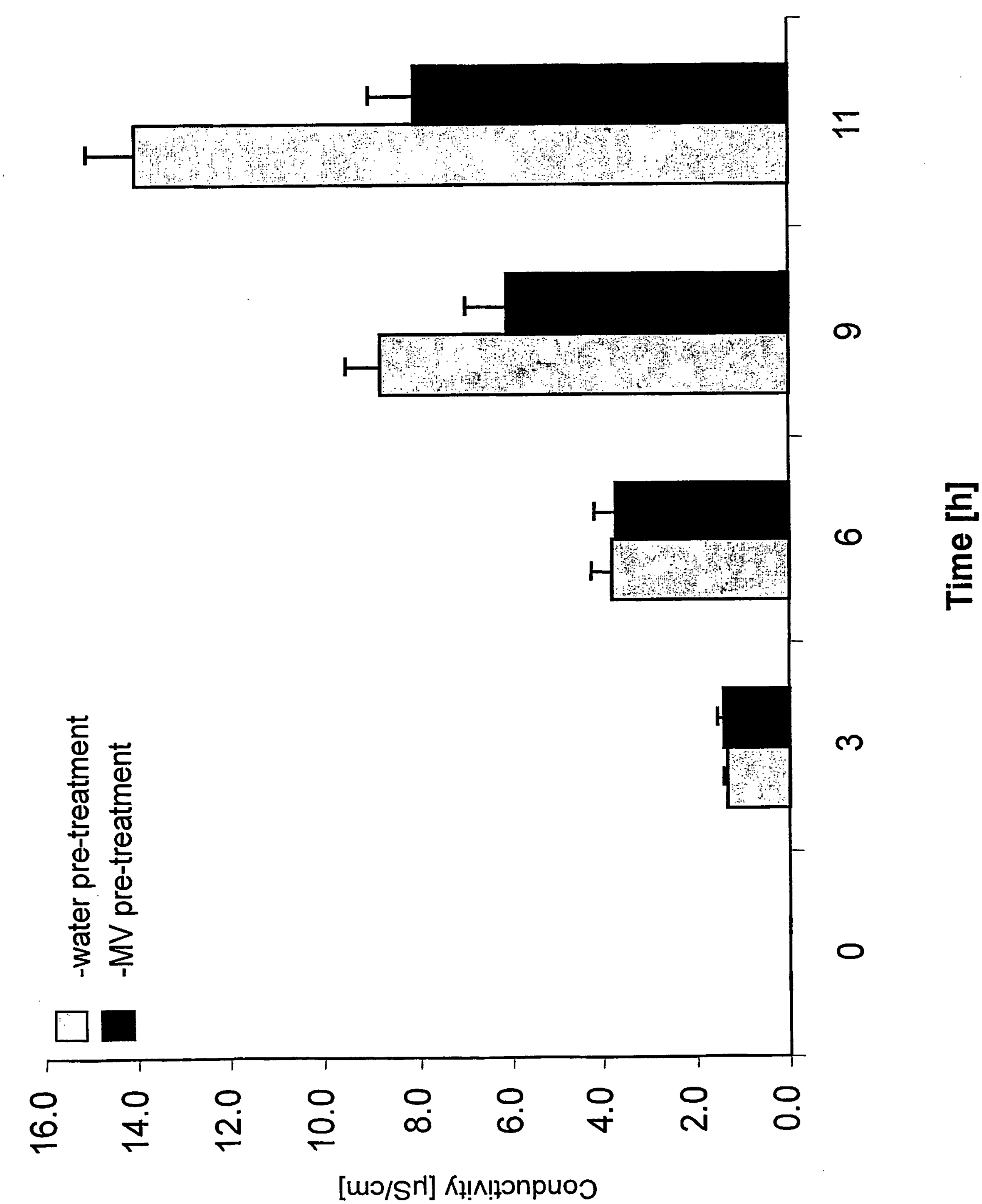

-water pre-treatment
-MV pre-treatment
Conductivity [µS/cm]
16.0
14.0
12.0
10.0
8.0
6.0
4.0
2.0
0.0
Time [h]
0
3
6
9
11

Fig. 3

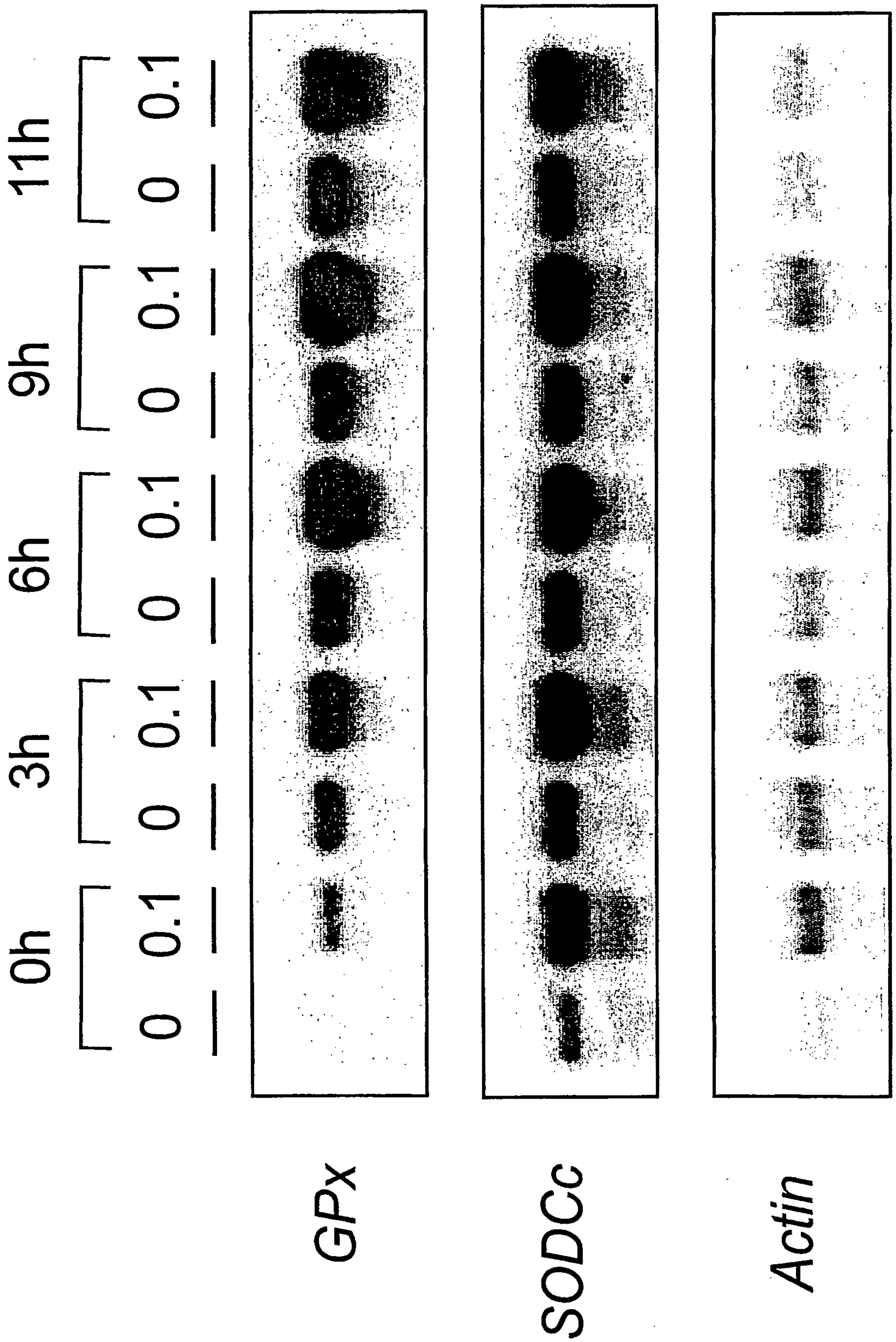
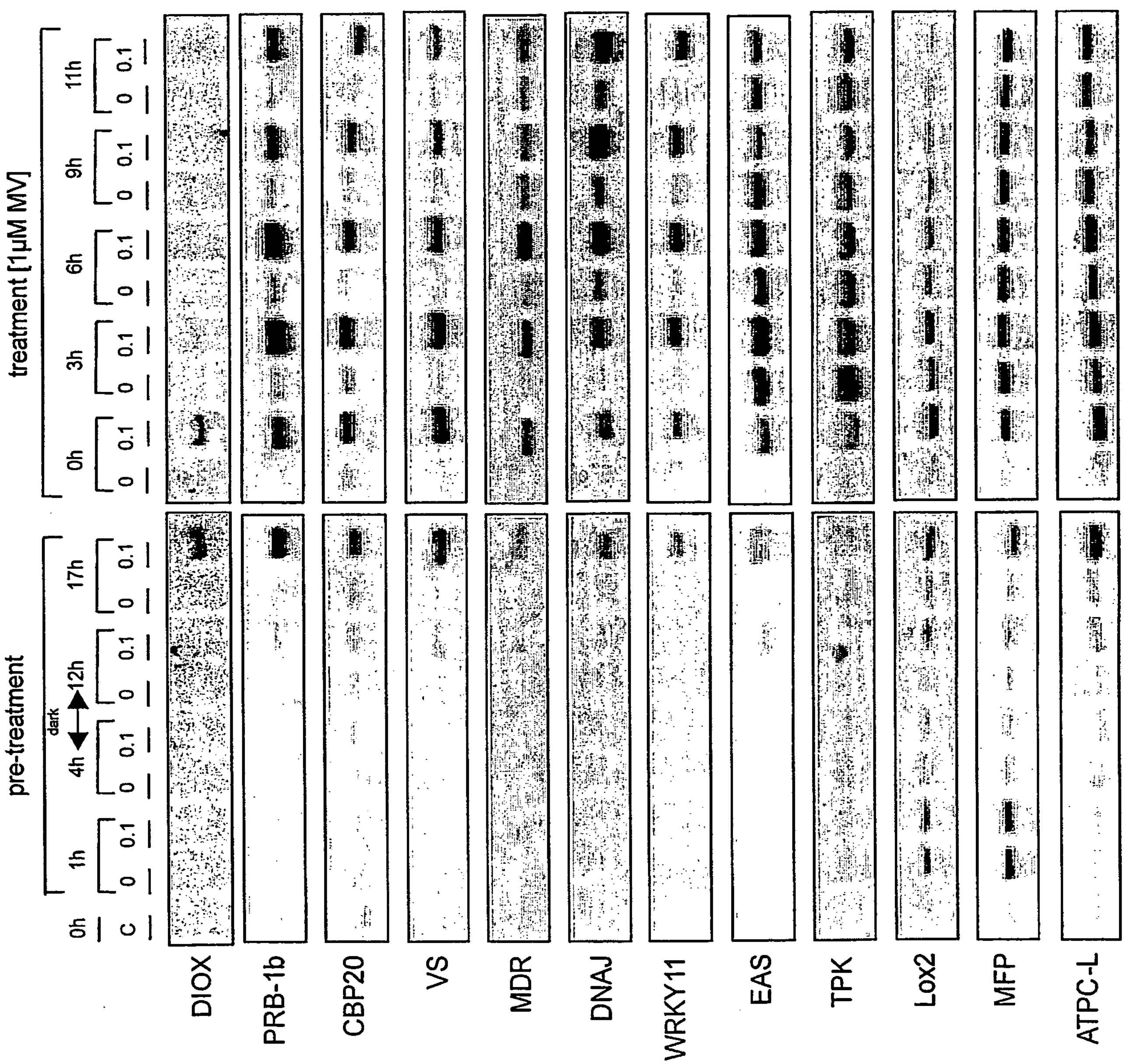


Fig. 4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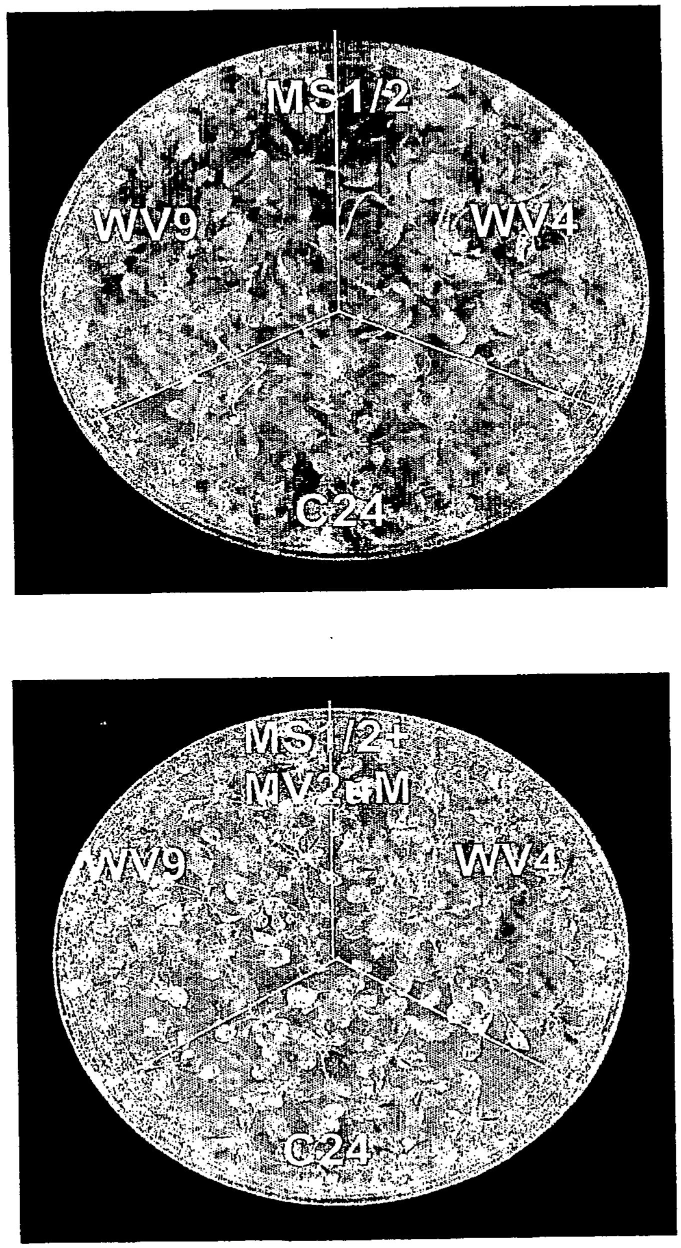
treatment [1µM MV]
dark
0h
1h
4h
12h
17h
0h
3h
6h
9h
11h
C
0
0.1
DIOX
PRB-1b
CBP20
VS
MDR
DNAJ
WRKY11
EAS
TPK
Lox2
MFP
ATPC-L

Fig. 5



SEQUENCE LISTING

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<120> Plant stress regulated genes

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<170> PatentIn Ver. 2.1

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atttagattc aggctcacag acttgacgct gctatttttt tactcagtaa gatcatcttt 180
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<220>
<223> homology with metallothionein, homeobox gene
induced

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gaggaaatgg ctgcaaatgc ggatcaaact gcacctgtga cccttgcaat tgttaagata 180
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taatatgtgg aaaagatgca tccaactatc acagatataa catccaaagg ctatacttaa 180
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ggtgccaatg gaccaaccaa aggcagcact cgaaatgctc cagaggtgga ctgctcaagg 180
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tgtagataca tttcaccttt tcaggttacc ctgaaatctg tcaatgaaa 349

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gttagagata acggagggtg acgacacgtg gtgggacgcg gacgccgtta caatcgagga 180
gcagtttgac ggttcaaata aaactagtca aattgaacga gtttcactga ctcggtgaat 240
gaatgatcta aaaagggtaa aatcgtaaat gacaaaggcg aaatgtgaag gaacgaacac 300
tcgtccgtgt ttgtctgtaa atataattat tttcaataat tattggaaat gataatttaa 360
tatttgg 367

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<220>
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ggaaaatcca gagggtaatg gtgttaagga aaatggtaag tcggaaaata atgttgtcaa 180
ggaaaatggt gatgttagta aaggttgatc atgaaatgat tgattaatta ggagttccac 240
ttaaaactag gatccaataa ttttgaatag ttttgctgtg ttcacattgt tgactttgtt 300
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cttgtgaaag taacattttc ataatttag 389

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ttcgggttgg ttcgaanagg tcgtcaattt cgccggagag ttcttcctcg tcgtcgtcgg 180
aaaatatttc gacaaagagg acgaagaagg ttgcccnnct atacagctga gggttaattt 240
gggaatttca aaattgttca attccatgaa caggttgagt tcaatatttt atttcatttc 300
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gtagaggggt ggacccatta tccgagtttc gaatgctgca gttgtnccta gacagatttc 180
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ctgtattttg caagngtagt tatatcttta atcttgtttc ataaaatgca tgtgtgattg 180
ttattttagt cgatagaaaa aagaaagacc cngtatagtt tgttgatctg tgctgcagtt 240
tttgacagcc aatgctgttt tttaggttac aatatgnagt tgattttcta ttg 293

<210> 12
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<213> Nicotiana tabacum

<220>
<223> plasmid a18-3-3 ; homology with EIF-5A (initiation
factor 5A2)

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aagagcagat tgccgctgtt aaggacattg gtaccaagaa ctagtcgcgc attctgcagc 120
ataaataatt tgctttagcc aagacatttt atatcttaat cgtggtactt tgatatccgt 180
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ttgggtgggg aganaagagn ntgattgttg cttnagcttg ggaatagtta cnaagtatgg 180
ttttctcata taaacccaca atgtgcatcg aatcaacttg tattgacatc tgactttgtg 240
ataatattca gtgtttatga 260

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tttgatttta cagccatctc tggtaaaagt tctgatttct ctgggctcag ttttgttaat 180
caatataaat caatataaaa acagcttgct tttctatgtt tnggttgatt tagatatgca 240
aatncttggt agagctgttt ctctttncc 269

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atttgagttc caagatttgg tgaagttact aaacagattt tgagttccta acttgtgcgc 120
aatgctggat aactcagcca ttttaatatt ctagtactcc attaatttat tgtttcttaa 180
cctatgtgta tgtttttcct gccgcagcaa ctttagttga tttcagagta ttcgttttga 240
tttgctcgaa aattgaaaag gacttgcc 268

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<211> 269
<212> DNA
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<220>
<223> plasmid a19-3-4

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aaaataacag tnctatcacg gaattactat tcaatcctca aaatgataag ttgtncaaat 120
aaatggggat tataagatnc cttttatctt tgcggaaggg ggtgattttg tatnctnggg 180
atgtgtaact gttgaataaa attgtgtgaa atccattgtt cataatgtac gaaatttcaa 240
aactattata tatgcgggac tttaattta 269

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<211> 265
<212> DNA
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<400> 17
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tattgttaca cccattcgac aaatatttca accaaaaaac agaacgtgac cttaaaagtg 180
agacaacttc tgtaaacgtc cacacgcctc aatgatagan taataaagcc aaccaattcc 240
cagttcccat aaccccaacc caacc 265

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<212> DNA
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ataaggcaag ggaaacattt cattcataga aacatgcaga aaagaattta tccagagtaa 180
taaaaactat taacctaaaa cgtcataaca aaatgagcct ggaataatac cctacagcag 240
taaaacttaa cgtccaaaaa cacaacacat aaaactcaac cacatcttgt tctgctggtg 300
gagtaaagta aaaaccaaaa aactaaaagg gggggttgag ttaaggggct tcatcatta 359

<210> 19
<211> 399
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid a3-2-2 ; homology with L12 (60S) ribosomal
protein

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caagagattg atgatggtga tgtcgagatt cctctcgatt gaatgcgaat tatcaactga 240
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(chlorophyl)-geranyl-geranyl reductase

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<213> Nicotiana tabacum

<220>
<223> plasmid a8-1-4 ; homology with an early wound
inducive gene

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caaagatcaa ttgtagctct ccgttaatat gtaaaataac ttgtgaatat ctgtatagat 240
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<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid a9-1-2 ; homology with epoxide hydrolase
[I]

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transferase [I]

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aaacatttcc ttttg 255

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gtgcttttta gcctattgaa aatcggattg cattttgctc taggcttatg atcttgtttt 120
agcttgctcc tattggtgtt tattttttan tatgttttat gtattaaagg naggattcag 180
agaataaata catattgttt atttctagtt ttgtca 216

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(lipoxygenase) [I]

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cctaataata atagaaaata aaatttttta tttttatttc aagggagttc cagctacagc 120
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gcccagtttt aaattg 196

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<220>
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taacactacg cttccac 197

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<212> DNA
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<220>
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tgttattctc gtctcagaga gggagagacg cacaacgaac atcaaaatag cgggagaagc 180
tcggaaaaat atgttttcat atatttatat aatttgaagt gaatttgttg tgttgaaaat 240

ttaactccct ctgtggattg ttattgaaga tataattttt tttcaatgtt cgttttctgt 300
ttcgattatt gaaagatagc aacagaaaga ttgtggctta 340

<210> 32
<211> 336
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c1-1-5

<400> 32
tgtatgatcg aggtgtaagc cctcttcctg ctgccaatgc agtagttggt ctgaggagtt 60
gacaattgat gacaggtgtt gacagttgat gattttcttt cctactagat taaagtctac 120
cttcactcat gtacatgata agcatttgta cagaacagtt atggttctgt ttataaaaaa 180
agattaggta gtcttgactt gcatttctgt gtattttgaa agtgcagact cgctctttaa 240
cttctatgcg tgttggcttc ttgggccttc tccttcttgc tcgtgattgc ttcttataaa 300
atttaagtaa aaatacatag cctggcattg ttcttg 336

<210> 33
<211> 400
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c1-2-2

<400> 33
agctacgann tgnctcnagg gcnngcaant gcgncgngng antnatngca ncnnngannt 60
antgttnnan ctggaacnga ntccangcaa cctgtttctg tggattcttc cacgtacctt 120
tggcttgttg atacatgtag atcgtattgc cgtcaacact taataacttg tacacgaaac 180
agcttctgtt ttgaagtctt tcccagtcaa tggtcgatag cattaatcgg ctgagatgga 240
gcttagatcc caagagtagc tgccttttag acggtttgac ctaatcgtgt gttttgactc 300
tattatgata ccttcatctg ctgcactaag aaattgacaa gtgcggtgaa tttcttacat 360
gaggaaattt caactggaat gccttagtat tattgtgttt 400

<210> 34
<211> 330
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c1-3-12

<400> 34

ggaatggatg atctgaaagc atcttaagtc taaaggaagt ttgcaactca gttgagattc 60
atccacactg agagaaactt ctgaaacaac catacttctg ctttatcctg ttgtaccatg 120
aatagctgta gcagcagaca atgagctttt tttaaagaca tttggtttgt aacttaaaac 180
ggaaggaact ggattgaggc aataagtgat tctggagaat agtgttttga ctcaaatatt 240
taatttcatt ttccagatca tgatcacctc ttgtgatttt acatgtttaa ggacttcaag 300
tgaatgtatt gttcagtaag tgttattacc 330

<210> 35
<211> 334
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c10-3-1

<400> 35
gagtaggatg ctggtgggat ggtcttctgt tttacagaat cctttacaga tctggtattc 60
aagaagacca tgtaggatgg taggatgtct tgagatgaag catgaattat cttacgccgg 120
aaattttaag aactttttgc catttttcat ttacagctca acagtttata tcgattagta 180
gatttagagc ttcctcattc catattctaa tccttccaac acattatcct agtctgtcta 240
gtattccttt tactgcattg ggcaaacttt gagctataat tgtactggtc ccaagcttca 300
aaagaatgta tgaaatgagc cattcactcg ttga 334

<210> 36
<211> 334
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c10-3-5

<400> 36
gnanagagng naantttggg ngganagntg ctgttgcnaa nccctanttt cncccngcca 60
antgnggaaa ggaattaata aaanaagttt ggattatnga acgtnggaag naacaaaatt 120
agtaattctt attactagtt attttcattt gttaacacca ataataacta atttgcttgt 180
ttggcttcat atctggatgc tcgcttgtgt agcttattat tgtcattgtt tgtatgaata 240
aaccaaggcg acgggcaact cttgactctt gtaaaaagta gacggtttct cagtgtagaa 300
gtcggagtag taccattcct gaaatcttgt cttt 334

<210> 37
<211> 216
<212> DNA
<213> Nicotiana tabacum

<220>

<223> plasmid c11-2-1

<400> 37
aatatgaagg ggggtaaatc cgtaaatata attaactaat caaatatcga ttacaaaatt 60
gtaagataat tgattgaaga atatccttct tttgtacata attattttca agattatata 120
aaatgaaaat tgatgtttga tcgagatgac tttccattat ttaagttgaa aatggagagt 180
ggttgtttca atataagtat tttaatctga ttttct 216

<210> 38
<211> 179
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c11-3-1

<400> 38
aagtgttaag taaaggtttc cattgcttat ccccggtata tttaccttat cattttctgg 60
ttggacatta ccgtgatagc tagaagataa tcatgttgac tgagaaatct tatttctatg 120
actgtaaaat ttgttaaaaa tgagaacgag ataagatttc ctattccgaa gcacatact 179

<210> 39
<211> 182
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c11-3-3 ; homology with caffeoyl-CoA
O-methyltransferase 3' [I]

<400> 39
ggaggataaa atatcatctt gtaaataaac tttactcaag ccgaatgaga caaattttaa 60
gtatttgtta caatttcaga agtacaatat ttgaaataca aatatataga aatattaata 120
gcgataatag tcatgagata caaaatattt attcacaaat caaaagaaaa acaaaggtag 180
tt 182

<210> 40
<211> 441
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c13-1-6

<400> 40

catcggatgg aggacaaggc aagtgaaggg gacagcaaga aacctcagag cagctcgaat 60
agacagactc ccacttcaaa tccatttcca gcttcttcgc aatctcctcc aattgccaaa 120
tccacaagta ataaaagcaa aagcccgctg cctccatctt tgccattgat atcagattca 180
acgtcgtcat cgtcgcaatc tcctcctata gttgccaaat ccacaagtaa taaagttaca 240
anaccgcaac ctccatcttc gttgatatca gaatcaaatt catcttagaa ttcttgatgc 300
agaatggccg tgctttattt gattcaccag tgattctttt gctcgatgct acaaaatact 360
agtaattaac taccactcga gaagccttgc aaattttgta tacacgaatg cattcaatga 420
actgggatcg accttctttg t 441

<210> 41
<211> 340
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c13-2-1 ; homology with L19 ribosomal
protein

<400> 41
agggaccagg agagaggcca gttcaacctg cagctccggc tgttgccgca ccagcccaac 60
cagctcaggg atctaagaag tcaaagaagt gagcatgatg aattgtaagg agggtgccaa 120
gcctgctttt tgttcttgct agtataacag tttagcatgt ttgatctgtt cccttattgg 180
tcttttaact ttggaagaca acgttacctg tacgaatttg gaagctggtt taaagttttg 240
ataccttgtt tctcagtgat accttttact catgttttga ttatatattc aacttagttg 300
ttttgcgtcg catggaatgt agtgagtgag cagctatttg 340

<210> 42
<211> 184
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c13-3-13 ; homology with 23S 4.5S rRNA
genes (chl)

<400> 42
ccagagacga ggaagggcgt agtaatcgac gaaatgcttc ggggagttga aaataagcat 60
agatccggag attcccgaat agggcaacct ttcgaactgc tgctgaatcc atggacaagt 120
aatgagacaa ccatcttgct gtatattata aagcataagt aataatccat tcttatagtg 180
agtt 184

<210> 43
<211> 186
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c13-3-6

<400> 43
gaagacaata caacattaat cacctttgcc tctgcgactt agagacaatt gaactactgc 60
attttgcttg attttctatg ttgtatcttg agtataataa cgtcgtgagt gagtttatat 120
ttgcaaagga tatccagtcc aatccatgct tgggttaaat gtatatttgc caaaaacttt 180
ctattc 186

<210> 44
<211> 549
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-1-60 ; homology with a glycolate
oxidase

<400> 44
ccttcaacaa ttcatggctc ttgaagaggt tgtgaaagct gcacaaggcc ggatccctgt 60
attcttggat ggaggtgtcc gccgtggaac tgatgtcttc aaagctttgg cacttggagc 120
ttcaggcatt tttattggaa ggccagtagt tttctcattg gctgctgaag gagaagctgg 180
aatcaaaaaa gtgttgcaaa tgttgcgcga tgagtttgag ctaactatgg cattgagcgg 240
ttgccgctca ctgaacgaga taacccgcaa ccatattgtc actgaatggg atgctccacg 300
tgctgctctt ccagccccaa ggttgtgaaa atgtacctca agtgtcaaat tgtttgatca 360
aagcaaagta ttgcttcact gtttcagaag cttatatttt ggttttgaat acttgtttct 420
gtttaatgag tttacgaata tgttaagctt ttctcagtaa tggaaaactg ataaattctg 480
ataaatggcc agatatgcct ccatttgtac atcctctatt tctatatatc atcatattgt 540
gaacttttc 549

<210> 45
<211> 49
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-2-10

<400> 45
attgctatac ttttccaagt ttgataatat gaaaagacat ttctgtttg 49

<210> 46
<211> 553
<212> DNA

<213> Nicotiana tabacum

<220>
<223> plasmid c14-2-15 ; homology with L35 (60S)
ribosomal protein

<400> 46
ggggaaaatc aaagactgag cttttggctc agttaaagga tctgaaagca caacttgctc 60
tcctccgtgt tgctaaggtc actggcggtg ccctaacaaa ctctccaaaa ttaaggtggt 120
gaggttgtca atagcacaag tattgacagt gatatcacag aagcagaaga cagcattgag 180
aaaagcttat aagaacaaga agtacttgcc tcttgacctc cgtcccaaga agactagggc 240
cattcgtaaa cgtcttacca aacatcaggc atctttgaag actgaaaggg agaagaagaa 300
agagatgtac tttccaatta gaaagtatgc cattaaggtt tgaattgatc caacttagat 360
agtttgtgat gttagagcaa agctgaggat cattattttt gccattttgc aatgttatat 420
tttgtattac tactattatt gcattatgaa gttggagttt tgttattttg tttgccttat 480
gcgtgcaact tttatgcatg atcctgtcta cacttctttt tctacacttt tgatcgagtg 540
tcgtgattat tgt 553

<210> 47
<211> 311
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-3-4 ; homology with L25 (60S)
ribosomal protein

<400> 47
taaaaggaag attaaggatg ccgtgaagaa gatgtatgac atccagacna agaaagtcaa 60
taccttgatt aggcctgatg ggactaagaa agcatatgtg aggttgactc ctgactacga 120
tgcattggac gttgccaaca aaattggaat catctaaant agtagttacc tgtttagaat 180
tttacgagaa tttaaaatct tggattgagt ttttagatac acttgaatgg aagtgccttc 240
tatttttcat tttgaatttt gtgttttgga gacatgtttt gttccgtata agagaaatca 300
acttttatgc t 311

<210> 48
<211> 272
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-5-1 ; rice genomic homology

<400> 48
actgggatag tcaaattatt gatcatgaag atgggccact cgaaagggag aagcttctgt 60
ttgcagtgaa atcatattgg acagcgccag ctgctcaagg atcttaaact acttaatccc 120

actgttttta atctttctta cttcaaagtc taatcatatt gctaatcctc tcttttattc 180
tttcacatgt taagttctag tattacttgc aaattgtaaa ctctaggatt ttaatgattc 240
ttcagcaact acactgaagt aatgagttct gt 272

<210> 49
<211> 270
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-6-11 ; Arabidopsis genomic homology

<400> 49
ggaagattat gctggcgatc gccgatggac ttggatcatc gccgattcaa atggttcttg 60
atgatagtga ccagaatatg atcaaacaag ctgccgatct cgaagcttct aagcgtcctg 120
cctaattaat tataactggt ttccagttct ctagcaaaat aagtcctttt tttattgttt 180
caattttcag tcatgtcttg tttccatgct gtgttctcaa ttctgtaatt ttacatactt 240
atatacaaat gaaatgtagg acaactttat 270

<210> 50
<211> 193
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c14-7-4

<400> 50
tcaccaaatt ggcttgtnna cttataatta ttgttagcat ataaaagaat aactattgtc 60
atattacatt tttccctaat gttcaatgcc tttttagttt tcaacaaatt caatgttttt 120
tggttcactt gtttgtgaga tgattgcaaa atcatcaatg taatgcagtc tatatttgaa 180
cgaaattcat tga 193

<210> 51
<211> 203
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-1-2

<400> 51
aagaaatcct gaataacatt tcatttggga ggaggtatta tatagttaat ggatttgggg 60
ttttttttgcc agtaaaattg tgttcaacat ttaatagaac tctgctgttg aaggggtttg 120
tttttatatg attagttact gtatttgtat tcaacagaca atattaattg aaatcaaatt 180

tctgcgtaga ccaacttctc ttt 203

<210> 52
<211> 492
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-1-4 ; homology with CBP20 (pathogen
and wound-inducible antifungal protein) [I]

<400> 52
ggacctcgtg gccgaaactc ttgtggcaaa tgcttaaggg tgacaaatac aggcacagga 60
gctcagacca cagtgagaat cgtggatcaa tgcagcaatg gcggactaga cttggacgtt 120
aacgttttcc ggcagctcga cacagacgga agagggaatc aacgtggcca ccttattgtg 180
aactacgagt ttgttaattg tggtgacaat atgaatgttc tggtatcccc agttgacaag 240
gaataagaag ctatatatgg ccatgtttag tctttgacgg cccaaataaa agtaaaaaga 300
acgatatgta aaaggaaaaa gaaaataaag ttgctttgat ggggttaggc aattccaata 360
tctattcaag aatgtctttc gttttgggaa gaaagagtga antgtgtatt atctttgtga 420
ttttgtatgc naatattgtg atttttaaac aaanaatcnc ntgggacagt atttgttggt 480
ctccttttga ac 492

<210> 53
<211> 201
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-11-2

<400> 53
ggatcatgag gtctatcgag tgaaggcaca tgcgatggcg agcaaaaaaa agcttttgcc 60
catgtctaga acacaatgcg gatacatttg atggcccatc tgaaaggaac tatactgcat 120
ccaagctgtt aatggccata atattttcca atatcatgac atttcttcac tgttattgga 180
taaacaagct tgagatctac t 201

<210> 54
<211> 199
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-11-4 ; Arabidopsis genomic homology

<400> 54

agttgtacac caaacttatc cataagtttg aaaccatttt atttccagtt tacatgtact 60
aaattatcgg tagatttgct tatatgtatt gtacagtagt tctaatggaa aggttgatgt 120
caatatctcc agagaggaca gaatgacgaa caaactgtag gtgcgagaat attgcttcta 180
aaacataaag tttcccgtt 199

<210> 55
<211> 431
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-2-8 ; Arabidopsis genomic homology

<400> 55
gtcgcacaaa ggcttccgtg gatacaatac catgaagtac ccaatgttgg acatttgctt 60
attcatgatc gagccgtgaa ggaggttatc tggaagacat tcttggccgg agagaaagag 120
cagatagtgt attcttaaac gggaagaagg agatttagag gttcctttgt aagaagacac 180
attctgtgtc ttttactggt atatcctatt gcatacatat taatcatata taaagttcgt 240
gagctagtag ctcaagtttt ggaacttcgg tggataatgg tttgcccctc taccctaact 300
gagaaatcct ggggagacgc aagtttcgaa actcgatgga taatggattt gaccttctac 360
ccttctttaa gacggttttg tggtacttga atgtgcattt cggtttaaaa cgttttaggt 420
gtggccttgt g 431

<210> 56
<211> 446
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-3-4 ; Arabidopsis genomic homology

<400> 56
aagaggaaca agtcatattg atcgctagat ttngcattta ccgtgtggat aaaatcctgt 60
nggagtataa tttcacttgg gacgatgtac tgaatttcag gctctacttt gcaagtagtc 120
ttaatatccc tcatagaaca ttgcctcgaa tcttcactga tgtgtttaat gaatttgctc 180
agatgagtca gagagttagc gtaaatgccg agcctatctt aaatatcgtt ccagtcttgg 240
gtgctgggag gtctttatcg accttggatg atatattcac gtgtgaattc atcgctagga 300
aatgttagat ctcatttaaa ttagggaatt atatattaaa tgttgagaaa aagagagttt 360
tgaacttgaa caaattctta taatgttatt gccaacccaa ttgttgcaaa ttacacttag 420
ctttacagga aatgaatata tgaagt 446

<210> 57
<211> 247
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-6-2

<400> 57
gaaccaagta aaaggcctga aatggaaagg aaaacaagca atcacaacta gacaacttca 60
acatagaagt gctttactac agtatttaag gacaaaatca ccaaaagcta atgaaaaaac 120
tggaggtgtt tgagcttcaa cactactcta ttggaaactg ttgtatgccg atactatgat 180
tgtgttttgg ataatatttt tgtggtgcaa gttatgatgt aatatgatgt aaactattaa 240
agcgtgt 247

<210> 58
<211> 325
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-6-3

<400> 58
accgatcaag tacctaatta gagttccaaa tgctgcttag gctttggtcc aacaaggtct 60
tgttgttcca ggcatttaac tccttttgt ggatatcgat tctttatccg cctgtgagtg 120
gatgcttctg tttttgccat cttctggaaa gtttagttga ctgtaaaaac agctaaactg 180
taaactaaat tagcagagga aatctgccgc cagatatttc aacatgcaag gatataatac 240
ttgtcgagaa taaaattttc agcttctatg gccttttctg tgatactttc aggaaaacat 300
tctatcagaa aatacatacg ttctg 325

<210> 59
<211> 235
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-7-1

<400> 59
gttgatgatg tgaagctctt gagtgtcagg aaccctcgtc gattcctctg agtcatgtat 60
ttttatgtaa aacgatgaat tttcgagtta tagtatgagt aaatttggtt gtaatgaagc 120
aaaaagaatg tggggagttc tgtttctctt agcttgttta ctagtagtgt tttcatatga 180
gtatgtatta tactaatgtc taatgaaagg caaagaagta tatatatttt gattg 235

<210> 60
<211> 307
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c15-8-5

<400> 60
taatgagcgt gacggaccaa atttagtata tagatagtac atatctttcg cattctagta 60
caatttatac ccatacaaga gtatacattt atgttactcc atacaaatga aagttaaaaa 120
agttattgaa tgtggaattc ataatcatag ggacaagcga tgtgaattct ctatgttttg 180
atgaacgact tgtatgatat gcttccttag aatacanaaa ttaaatatat ttattgcnaa 240
aaaaaaaata cntgactcan aggaatcnac gagggttcct gacnctcaag agcttcacnt 300
cntcanc 307

<210> 61
<211> 342
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c17-3-1

<400> 61
aagaatacaa gtactgcatg cacaagcatt ccctngggca gagcttggat gatattaaag 60
gttccttcga gtggtaaatt ggcaaaatct gctagcgtgg cctgtgtacn cctgcatctt 120
ttcccattaa caacttcctg ttgtatgtat tgtgtcnatc gtgtggatgc tcattgattt 180
gtactaatct gtaacgaagt gcaactttca gagattaagg ttttgttttc catttcngtc 240
ccntggggtg ttccggaaca actatggttg cttgtaaatt cctctgatct tgacagtggg 300
ggcaatattc ttacaaattt atttcaattt caaccggtta ta 342

<210> 62
<211> 287
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c17-3-5

<400> 62
ataatgacgt gtcataaaaa atgtgatgtg gatgacgacg tgtcatccac antgtgcatt 60
tgaagaacac agaggggttt aaagtagtgt gtttttaaca actacgagtg ncttgataaa 120
agcttgtgga gtataggggc cgagatgaca aatcaggaca agtaaaggta tttattaggc 180
tattatgcct taattattta taatttgctt aaacaatgtt tttaaaaaat atttacagct 240
attnacttgt atatcagacc tttacatgaa tttagcttat tgttttt 287

<210> 63
<211> 211

<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c17-5-5

<400> 63
attactattg agccttagac tatgatggat atctataaga agaacaagca aagcttgggt 60
cgcttatggt ggcctttgtg atttacattt tactctactt cgaattttca attaatttga 120
ttatattctt ttgattagtt tagttctata cttaacttgg gattgttgat ttactttgac 180
ctcttcactt agtattctca cttagttatt g 211

<210> 64
<211> 211
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c17-5-8 ; Arabidopsis genomic homology

<400> 64
attgaagagg attggggaaa ttcctgctgt tgaggagttt gtttacctta aattataaga 60
actgtttgat ttctgtctga attcgctaca aagcaaaatt ttgatgatgt tatttgttta 120
ccagtagtag tctagtgcag gatacaaaaa taatttggat gtgaaattag aagtgtagta 180
catttggttg tcaatttgac aatctttttg g 211

<210> 65
<211> 187
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c17-6-2

<400> 65
gatagtctat tagttaccca aacctgctcc gtatattttg catattgtca aagtgatctt 60
tcaggtactt cgtgattgtt gtattcattc taaattttgc gatcaaaata gttcatcctt 120
agtgattgta caantaatac taaaactggc actatttngg tttgaattca cantttctca 180
cataatt 187

<210> 66
<211> 382
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c18-1-2 ; homology with DNA-J domain
containing protein

<400> 66
cttgataaga ggatggcaaa cattcaaagc cgcacctcga gttcggaggt ttnatcccgg 60
tggtttgaac angttatgac aagaagggaa gcagcattaa ttcttggagt cagagaaagt 120
gctgtcctgg agaagataaa ggaggctcac aggagagtaa tggttgcaaa tcatccagac 180
gccggtggta gccattatat tgcttccaaa atcaatgaag ctaaggaagt cttgttaggg 240
aaaaccaaga cagctaattc cgctttctaa ttcaccattt tgtttgcacc ttccttctta 300
acagcttaat tgtccgtata cgtgtaacaa agtgaatttg tatccgtaga catgttacta 360
tcataattta ggagacttct tt 382

<210> 67
<211> 340
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c18-2-1 ; homology with CCT (chaperonin
containing TCP-1) beta subunit

<400> 67
aatatctgag tcgttcaaag tcaaacaggc agtgttgctc tctgccactg aggctgctga 60
aatgatccta agggttgacg aaatcatcac ttgtgcccca aggaggagag agggaatgta 120
aaaacaatat tggtcatgtt taagctgttg agatgactcg tattttatta tggtttgaga 180
atttgagatg gtaggtgtgg gctgtaaacg agtcaaatga tagattgcta ttggaaccat 240
gctaaagtgc actgcgctga gtagtttctt ttgaggagca aatgttttgg tttgttttca 300
taatgtatgc atgcttctat agaaaacatt tgttcgatac 340

<210> 68
<211> 336
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-2-11

<400> 68
aaataaggtt gcggaagcaa acaatccagg acattctgct ggatcattgg tataccgtaa 60
tgaaggtttn gttantttgt ttctgtggca ttgttcaaat cttttatcag tnctccgctt 120
ctatagaggc aaaagggaat cctttctttc agcatgtacc tgtaataatt tgtaaaaata 180
aaagttgata agtcatgtag ctagctgtgt taatagaaga aagagatgag agtgagattt 240
agtatagatg ttttatctat accttnctgt ggtatgtagg cttttactgc tcanctcata 300
cctcattgac acatctaatc aaattattcc acttct 336

<210> 69
<211> 338
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-3-10

<400> 69
caggcaacta ataccaagcc attagtttct cattatgaaa aactttacaa agacaaaatt 60
acncanaact acaagccaaa aaagctcaac atagtaactn tgatcaaatg atcatataat 120
atttgcagcc ttggacacac ctcagcaaca gaatggaacn tcaacaacac taanaanttg 180
cacacctaaa tccaaaacaa aaagactcga ctccgtatca naaantangg tttacntgaa 240
aatgtatgat ggtnancaac actgaaactg tctaacnant ataanttcnc nctctcaana 300
caancnttat ctctgttcgt tnanccgttt ggttttat 338

<210> 70
<211> 323
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-4-19 ; Arabidopsis genomic homology

<400> 70
actaagtttc tgcatttggc ttgatttctt atcaagttga gacaatattt gtcattacaa 60
ggcattttta gtaccaaaaa aacattagca gtaactaaaa antatanctt ctggtttggg 120
gggattcanc aatttgaaga ntctgttcga tgantttaca agctttcttg ctcctaatct 180
ccactctcat gctttcactc ttctcaatct tatcgtaaga ttccttcatt ttcagagacc 240
tcctcaattt tgtcttcaag ttcatcatta atctctcaaa tcccatcatc tccactctgt 300
atttcttctc aatttaattg cct 323

<210> 71
<211> 326
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-4-22

<400> 71
taaaggatat tgaaaagtaa atcctgcaag cacatataaa ggtatgtttc tacaaaaaca 60
taaatcgtat aggtagaaat gaaaggcggg ctgagaggga aagtgcagca nagtgatctc 120
ctgataggac ttctgaacca catnctacgt nggctttaaa gcactcaaag ccactactgg 180
agaaacagca ctctccactt gtatctcagg aatgcactat aagaaaatct antatactan 240

ctggacaata taataggtag gtatttaagt ggaaaagggt aaagggacaa gcccattatc 300
taccatgttt tgaactgcgc acncgg 326

<210> 72
<211> 256
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-5-1

<400> 72
atatacatct ggagcaaatc acgantttta atacaaaact caccctacaa aacatggant 60
cnccactgca tcttaggcat ntggacagca anaaaacaag caanttgttt ggccgcctnc 120
actatttaca tttactctat tttgaatttt ttaatcaatt tgattatntt atttggttat 180
tttanttcta cacttaatct gggattgctg attcagtttn gacttcttta cttagtattc 240
tcacttcgtc actggc 256

<210> 73
<211> 257
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-5-4

<400> 73
atttaattga ttagcggaaa atctnctttt gtttnggttt atattgcaca ttctcatgga 60
tatttttact atttgtttca tagtttaaca tcagcaagtg ctttcttatt ctggtatatt 120
gacgccaatg tantaggctt tgactttctt ttaaacattg ttgttgttga catctaaagg 180
ttctctaaat ttgaatttnc actcttcaat ttgcttcctt tgaatgcaat attgctcgtc 240
agctttgcat ctttgtg 257

<210> 74
<211> 242
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-6-3

<400> 74
caaactagga tgtctgaaag actgaaagcg ttagaagtaa ataagtactc atttacagcg 60
gctgggtgtn acataccaaa acaaaacatt caacaagatt gtatccaaaa gaatacctgg 120
aaaaattaca acacttggga actgaanaac cttanctgac cccagaaaac cattaaaggt 180

aatatagcgc atctttacac ggttgtgaan atcacaaaat atcctcaatt tgttgcctaa 240
ct 242

<210> 75
<211> 257
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c19-7-4 ; homology with putative
translation initiation factor 2B beta sub. NIFb

<400> 75
ataaactata ntaccattta gttgttgata atacgaatga ataaaccatt cgacaactta 60
acttttcagt caacaatagc atacgtgttg tctaataata ccacaaagga aaaccaccat 120
caagtagtac tctgcatatc cgaaatcaca aaactccagc acaaatctaa tctcanaatc 180
aatctacaaa ctccaaaaat cgcgatgctc tcttcatctg tttattgcag tcagtataat 240
gtaggtgcaa catcttg 257

<210> 76
<211> 384
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-1-10

<400> 76
gtgcagtaaa ctgaataggt tgacagagct agctgccaga tgactcttca tgcggtaggg 60
tttttcttat attactgcca tacagtattg gagctggaga tatcaagacc gtgctagctc 120
tgctgattag ttgtccgtat agatgacagt gatacataag ctgacttgga atccaagtat 180
ctggtctacc acaattgatt ttctttggga tttactcaca atattcttaa acgatttttg 240
ccggataaat gcaatattca ttgattgtaa tcaatcacta caaggaggat gaagaatata 300
ttcttaaatg atttttgcca gataaatgta atattcatct atatggatag atgaattctt 360
gatcaaatgt aagttcatgt cgat 384

<210> 77
<211> 181
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-11-14

<400> 77

tgatgcgcat atcaaaacta attattatcc aagccaaagc tatcctttgc cagttgcttg 60
ataacacata tcttttgtgc ttgattttaa aatacatgag gtgtatttgc cgttgagtca 120
tattgcagcg gtgttcaatg taatttacac tgatacaaaa taaggtaatt tgtatattgt 180
g 181

<210> 78
<211> 182
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-11-2

<400> 78
aggaaatact gcatcaaacg gacaacaact cgatgcaggt gaagaatcct agtgctgtaa 60
ttgctaataa caagcacata gtttgtctgc tgtcttttta ctttaatatt ttcccctttg 120
aagttgttgg aatcgtatta attttgttag ttaaaggcgg atcaatcaat atatctttcc 180
tg 182

<210> 79
<211> 359
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-2-1

<400> 79
aacgggatac tgaatggtag gacggcctct tcttcgacca ctagcaacca tgtagccgac 60
caagttcaaa gatgaaacat actgtatttt gccagtggac attctttttg tgtggcttat 120
ccttataggt ttttgttcat tatctctggt attccttgtc aaagtacatt atgatggcag 180
acctctttag agagatcctc aaagtttatg tgttgtttat ttatatcatt ttttctcgat 240
agttaaatat taggggatat tcttctttcg gccatttgat tttggttgaa ggtcttgaat 300
gtcgcaagaa atagctcagt ttaaaggagt tgatgaatgt tctctccttc tctgccgcc 359

<210> 80
<211> 356
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-2-3

<400> 80
agaaatatag ggtaaggctg cgtataatag attcttgtgg ttcgaccctt ccctggcacc 60

cgagcttagt gcaccgggtt gccctttat ttcagaagat gtatattatg aactcttggt 120
ttagattgag ttcagattat tttttaagaa attatttttt agcaaagagt aagctcactc 180
tttgttctta ttagtaataa gtttgttaag ttatcctttc acaaatgata tacagtattg 240
gtgtgaggtg tgtgagggtc atattcttgt gtattaattg ttgcaatgca acgtgtaatt 300
gctcaattgg ccagattggt tttctcttct taatgctaag cactacttgt tatcat 356

<210> 81
<211> 338
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-4-1

<400> 81
gtggtttccg tgaatcgtga cgccaaatat cagttagcaa tggtaactaa ctccatggca 60
acatactgga aatgagtgtg aaatctgaat ttcagagttg gtgtgacttc ttcttgtata 120
gctggtggtt gttaacttgt cctagattca ctctcactct cattggtgtg gtccctgtgc 180
tagtgacggg tcttattgtg gctctttaga gttgatgtta tatttactct acctatctgt 240
tgaagtttat ccaattggta tactttttt gggttgtttt aacaaagtgc tattcgaatt 300
tgtaatttca atttcgatca aaccacctta aatctgct 338

<210> 82
<211> 336
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-5-6

<400> 82
ggtggcctaa tttgcagttt tgatttagtg tcatcattag ctattttctg gattgaagtt 60
aaatgccgga aatctgtttg taacctcaat cttcaacaaa tcaattgaaa tatcacttca 120
aggcacttca ggtcctcctt gcacgggttg agagcttcca acagatttcg gagattcact 180
aggtagctgc ttggcattcg cagcccaatg cttctccctc tatcttattt tctcctattt 240
tagttctgta atagactatg tagactcttt ctgttttaaa tcggttagta gatattcatg 300
actggtgaca ccccgttgtc gggctatgtc tatttc 336

<210> 83
<211> 256
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-6-5

<400> 83
ttaaagaatg ttttgtctaa tcttgtgctg gctttaatgc acgtcaaagt ttgctgtcat 60
cccctggcaa tagcggacaa caaatctgcc agctactgat gctgatgggt atttgtttaa 120
gtggagaagt aaataggatt ttatatctaa tattattgcc tttcatagtt ctcagagtat 180
atgtgtagaa caagcacagc tgcaaattgt tattactaat tttatggtgg aaatctgttg 240
aaagttattt tctttt 256

<210> 84
<211> 254
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-7-1 ; homology with patatin 3'-strand

<400> 84
atgatgtcgg ttttgcattg tggaaatgca agttttactt tggcagattg ctccaagtcc 60
ttagggggtg atggatttcc cctacaacag aattactatt tttcctttct ttttatgttg 120
ttttggctta gaaggatgat tttatttatt taacacaacc aaaagtctac ataatcctta 180
gcatatttca aatttacata gagggatatt tctattgaaa tttatccctt aacgttacaa 240
gcgcttattc ttta 254

<210> 85
<211> 219
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c2-9-14

<400> 85
gggaatacat tgggtttgtc gtttgtttgt ttggatgtta gtagaccggc aagatatcta 60
gcattttgct tctgttaaca tggacattat ggatttgtaa attcaactga ctacttgtac 120
acgtctctct ggacattcgg gttattactt ggtacaagtt aataacactt atgctctctc 180
ttattttatg ctttctgatg aatattcctt ttccctctg 219

<210> 86
<211> 337
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c20-1-4 ; homology with DNA-binding
protein (pabf) [I]

<400> 86
gaagatgcgc ttagacttgg aggcagtgta gctacctacc tctaatgtca atttgttagg 60
ttaaagcagg atttgatatt ttgttgcaca gtatgaagta tgttttagtt ctaactgtat 120
tagcagttga tttcgtcatt tgataattac cttattctgc taatttggtt aatgacaatt 180
aaggggggaga caaaatcatg ctcgtgggct atatgtactg ttgtttgagt atgttgaatg 240
gatggaaatg cctttgttag atagatgtat aatgccggca ttatccctca tcaacagttg 300
cctttgcaaa tgtcgtaaaa gcatttgaat tttattg 337

<210> 87
<211> 337
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c3-2-4

<400> 87
aaagcaactc cacgttagtg ttataaaacg agtttaataa agtttgactc tgatactatg 60
tgaaagaatc taagcactaa aacaaaacct ttaggcaata gtataacatt gagatgtttc 120
ctttctaatt taaagaagga tagaagttca gtgcactctg ctcacaagat gtagtacaag 180
gattcttgaa ccaaggattt tgatggactt catgttgaga ttggaaaact gaattcatta 240
ctggagatca ttgttcatgg ccctataaat ttgaaatttc aaagatacaa atcaaattac 300
ttatatgtgg catacaacaa gacactacta atacata 337

<210> 88
<211> 92
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c3-3-6

<400> 88
ggttgaccgt gcttaatata ggcagggagg ttgataatta tataaagcac atctgaatgt 60
taatccacgt aagaacttaa tttgattgct tt 92

<210> 89
<211> 257
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c3-4-1

<400> 89
gcatagactt ttttccacca tcagattagt tggcttgcga taagagacga cttcttttag 60
caaatctata tgataacctg aagaatatag taagaattaa tctgctataa ccagttaaat 120
agtactaatt acaacttttt ttttaaagtt gtttgttaaa catttttcat gccattttgt 180
ttgtcaagta ccgaaaaaac gtgggttggc tacaaaagtc ttaacctggc tagctagcta 240
cctgctactg agtatct 257

<210> 90
<211> 345
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c4-1-2

<400> 90
taatcaaaat tggtaaaaca atccaaacca aaaaaaacgg tttnntgttg ctcttgtttg 60
aaatatattc gaatgttcct taatacctag cgtatgtaat aataaaaatg tactcttgtt 120
gctcttgttt gtattgggat tatttaatta tatttgagat ttataattta ttaaaggcta 180
atcgaatagt gttgactgat gtttggaaaa tgtcatcaga tatcaatgtt ggaagccatt 240
tagctcagta aaattatttt aactaaatca aaagaataaa atactatagg ttggagtaaa 300
taagttgtta atggtagtgt ttttctattt agtcatttgg gatta 345

<210> 91
<211> 193
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c4-3-3

<400> 91
tactcacggg gattaatctc atcacggttt caaatggaca aacaattatt ttacatggag 60
agtagagacc ctccagcttc tttttattgt tagtagtagt gtgaattctc gtgttctcaa 120
tttggatagt tatggtttct aacttatgta ttagatcatt ttaacaagca gcacagagat 180
caaattgttc act 193

<210> 92
<211> 340
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c5-1-2

<400> 92
aaactagtgg tttatttgtt tcatcgtgaa tatggagcag ctgcaataat atcttcacaa 60
tagtactcat tgactagatt tgacacttcg gatgaagcca aggcatcttc agagttttgg 120
attctacaat gtttccaagt tatatctgct tttaatcgtt tctgcttgta gcttaattgt 180
cttttgatgc tgtataccgt gtccaagtat gattgtagtt ttagggaatt tcagattgca 240
aggcctttat ttactcggat caaatttgta attgctagtc cccttttttt gagaaattct 300
gtatgtccca tttctttctt ccaatggaac tttcacttta 340

<210> 93
<211> 343
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c6-8-13

<400> 93
agcagaaaga caagtgtggt tctggagcca tgaaatcgcc cgagtactct gcctcctctt 60
gttctggtcc aatgcagttt tccactggtg ttgctgtggc gtaagtcttg tatggtacgc 120
aactcaaact aataaataag gaaactgttt atacagcttt tggaaagcta acccaataag 180
atttggtcat aagtagatgg gttatgttca gttttgagca ggcaatctct ctgaatggaa 240
tgttgttcag cctgccccta ttgagaggaa gaggacttct tatttttctt aaacccatag 300
acaagttcat ctataaaaat taatcattat tctttctttc ctt 343

<210> 94
<211> 337
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c6-8-4

<400> 94
gataggtatc agatggacct tataagtgag aaaactccta atgcaatcat ctttacttat 60
tggaaatatt tatagtgtga cagatacttg gccaagtgct acagttatat gtactattta 120
atgaacaagt tttatggtgt ttggtatatg atgtaatttg ttacttcaga atttattctt 180
ctgagtgttt cactggtagc atgatttaca agctaattgt atccattttc tgagggatag 240
gatacagtta gattgctttt caatatctga tttgacactt tgccctatga ttcttgtttt 300
ggaatggata caagcaagct tattgctgtt ctgattg 337

<210> 95
<211> 294
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c6-8-9

<400> 95
atctacacga gcttcgtatg tgtaagacta ctggatcaga ttatccactg ctctgatacc 60
atattaaaat cagtgacgta atgaagcaat tgaactcgag gtatgctcca attatggaaa 120
tggaaacttg gcgaagaagc cccaaattag gggcatgtgc gacannngag aagaagagaa 180
cttagaagtg aaagtctcaa ttgtattgac tatgtaatgt cgtatatatc agtgttttaa 240
aaggtgtggc gtaaggctag gcattttaca catacctcag cggggcgtaa nata 294

<210> 96
<211> 338
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c7-1-2

<400> 96
caaaggactg tgcttcatag tggtgctggg agaggtnttg cagccactga cacatcaagc 60
accaacgagg aaaaggaatt gaaagaaaat aataaattcg atgtaggatc aaatttctat 120
ttggttgggt taattttant gaagttgata ctgcaacagg agaatgacag tcctttgaaa 180
tttnaagtta ctattaatcc aacaagagat tgcgaatatg ggaggtatga gatnatctct 240
gtttctttac cgtcctttac atctgaaggc aacttagcat aggagttctt aaatgtatca 300
aatatcaata ttttcagcag agttcatttg ttctttat 338

<210> 97
<211> 341
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c7-1-6

<400> 97
agtgaagggg gcaagagaag aaaaggaaaa gaagaaaatg tcagtcacaa acattcaagt 60
gtttatatgt attcaacttt tatactttct ttcaaatgat ttttactttt gcagatgggt 120
gaaagaaaaa gaaaagagtt tttccaaact cgagacagaa aaagaaaaga aaaagcattc 180
ctctcttctg aatcttgatt gcgtctttgg tgtttgcgga caaatgtcct gagatgggtg 240
aacttcacat ggtcgcgtgg tgttgtgctt tgtgataaaa tgtattgtgt atttatcatc 300
tttctactat aaatcgaaat tttattaagt tgaagtcgtt a 341

<210> 98
<211> 314
<212> DNA

<213> Nicotiana tabacum

<220>
<223> plasmid c7-3-10

<400> 98
atagcatata tatgttgaag cccctgctcc caactcaacc ccctcctttt cttacagcca 60
ttaatatatt ttggaatagc tatttcctat tttaggaaaa aacgaccatg tattgttcat 120
tgacaagtac tttcataccc tgctcaaagc aatatgtgtt ttctcgtact tggaagttaa 180
ttttgctgtg gaacaactct tgttagctta gtgttgtggg gtgagctata actcggcctg 240
tgtgatttgt tacatttggt tgagcatttt ctcttatata agaagagaca gtgaggtgtc 300
tgtctcatgg tcag 314

<210> 99
<211> 276
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c7-3-3 ; Arabidopsis genomic homology

<400> 99
ggctgagaag aagaagcgca aagctcagtt gcaggaggcc aatcggaaaa aaatgaataa 60
gagagtagag cgtaaaatgg ctgcagttnc tagggataga gcatgggcag aaagactggc 120
agaactgaag aagctcgagg aagagaagaa ggcagccatg gcttgatggt tattgaacag 180
agtttngatc tgttaatttt ctctcttgtt tttgagagtg aaaaatatat taatccctta 240
tttaataggc acaattttct tcacacaatt tttatt 276

<210> 100
<211> 418
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c7-3-9

<400> 100
acnaatnaga antaccacgt gnantgtcnt gntacngtna taagngaaga ggttcgatcc 60
ngntcatcnc aaatgncant ggccccgtgg naagctcagc cnngacaccg gantgtttgc 120
nngnggtntt attacagcta anntttattt ctccaaangn gataanagat ngttctgtga 180
nnaggntnng attgnatccg ccggaganca gaaagtnatt nttgcatcat anagtnggtn 240
agangtgact cccntntctn tgtcngnata tntntattgg nggggntnt tttagnattc 300
cagtncattc cganatatag atcncanatt ncnatanntn tacnanngcg cccccgcncg 360
nntgtannnc atnngggaga tctcccanac gaggccggan gtagagtgng aaaatctc 418

<210> 101
<211> 244
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c8-1-5

<400> 101
ggaatatgca taattttgtt ttcttttttg tttaaaagag ttcaacctag ttttatctgc 60
cagaagagag aaacatcaag atgtgagcat cagacaagct tataatactc tctctatata 120
gatttctaca aagcttattt ttggtgaatg cttgtgttgt gtgtaatact tcaaccccat 180
ggaaatgcta cgtttattag ctcgtgctgt ggcacccaaa tgaatcttga ttgtgtcatg 240
ttct 244

<210> 102
<211> 346
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid c9-1-4 ; homology with Drosophila heat
shock protein 82

<400> 102
gaagtcgagg accgtgccca acggtcagca attacaagag taaatgcaga tgatgttcgg 60
gtcactgtat ccgcacctgc agctcgtgga gaagctaaca atgaacttat ggaattcatg 120
ggtcgagtac tgggtctgaa actatctcag atgactctcc aaagagggtg gaatagcaaa 180
tcaaagcttc ttgtagtgga ggatttgaca gctagacaag tatatgagaa actcttggaa 240
gctgcccaac cttgagatgg ctccctgatc cttttcttct ttgtcatttt ttccatgttt 300
gtaacattgg atttttagtt tcataaaatt gaattcagtt gtcttt 346

<210> 103
<211> 360
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g10-1-1 ; Arabidopsis genomic homology

<400> 103
gaacgagaac aaaccatctc aaaagtacat cgagatagtg actgaagata attttgaatt 60
ttggttcatg ggctttgtac gatatgaaaa agctttcttg aatttacaaa aggctatttc 120
catcacgaat tagctagctg ttaggcatta gaatttttag ggttttaaag aggattcata 180
attctgtaat tgttcttttt tccttattaa atgttgaact ggtagcatct aatctatgct 240
tgttcatcat tttcttttct ctcaacggaa gaggatttga gatttatgag aattgaattt 300

tgtagattct gaaatttaat gaatttctca acatatatat aagatttaga ccaaagttac 360

<210> 104
<211> 556
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g12-1-21 ; Arabidopsis genomic
ABA-regulated gene cluster homology

<400> 104
ggtgggattt gactatgcat atcgcaaagc aatgaattcg actatgaaat tcatcacaag 60
ctcaaagaac aaggcgtata catttttag aacgactacc cccgatcact ttgagaatgg 120
tgaatggaat acgggaggtt attgtaatag aacaggaccc ttcaaacaag atgaggttga 180
cattggttat gtagatgagg tgatgcgcaa aattgaatta gaagaattcg agagtatatc 240
gagaacagaa tctgcagaca ggttgacaat gaaattgttc gataccactt tcctttcgct 300
gctgagacca gatgggcacc ctggagtcta caggcaatat cagccatttg ctaaagaaaa 360
tatgaacaaa aagattcaga atgattgtct acattggtgc ttgcccggcc caatagattc 420
gtggaacgat gtaatgatgg aaatgttgtt caccagttga aaatggtgtg acattagatt 480
ttgattttgc tcccacaatt gtattgttca tctgcaaaag atggttgcac actatttttc 540
accattgttt cctctc 556

<210> 105
<211> 579
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g12-1-5 ; Arabidopsis membrane related
protein CP5 homology

<400> 105
tattattcaa gttggtatat tggagaagtg gaatcaagta gaggtaacag ccagccgacg 60
cgatgtgaag tgattctatt ccatcatgaa gatatgggca tcccatggga aattgcaaaa 120
tttggggtaa agcaaggtat gtggggagct gtgaggaaga ttgagcgggg attccgtgcc 180
taccagaaag ctaaagcatc tggcttgaaa atatctcatt gtgcttttat ggctagagtt 240
aatacaaaaa ttgatcgaga atacttgaag tcaatggaag atgatgagga ctcatctgaa 300
actgaattgc aagcttcacc tgcaaaacct gagggcatga acataccaaa gctgattatc 360
attggtggag ctgtggcagt tgcttgtacc cttaatcaag gaatcttacc caaggtgctt 420
ttgtttaatg ctgtgaaaag gtttggaaat ataggaagga gagcatgtcc aaggacatga 480
catttgattc atgcgtgcat tgcgcatttg ttttttccct gtttaagcat tcacttttaa 540
gctctttata tatttaaaac aagcaagtgt tattttgtc 579

<210> 106

<211> 358
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-2-4 ; homology with vetaspiradiene
synthase PVS4 (sesquiterpene cyclase)

<400> 106
gatagcatgg aaggatgtga atgaaggaat tcttcgacca actcctgttt ctacagaaat 60
tctcactcgt attctcaatc tcgctcgtat tatagatgtc acttacaagc acaatcaaga 120
tggatacact catccagaaa aggttctaaa acctcacatc atcgctttac tggtggactc 180
cattgaaatc taaaccattg agtgcttttt tcatctcggt gatcgtttta tttttatttt 240
taaataaagg atcagaactg tgtttctgtg ttcctcttta tataagcaag ttgagtttcc 300
tacttctgtt caaaccctgt gtttgttctt ggcgtctgaa taatataatt ttgtttgc 358

<210> 107
<211> 264
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-3-10

<400> 107
caaagataaa gaaggctgga gttgtaagac aggagcttgc taagcttaag aaggacgctg 60
cttaagaact ctttgattag tgagatttgt atgataggag ttttggaagt cgttgtgttt 120
tgcttttaga ttttggttca ttactggcaa gtcatttggt ttcatctttg gtgtcattga 180
agactcctag aaatcaattt cccaatagtt ttcatttgnn ttatgatggt gaacattctc 240
ttcgcagaca cttcattttg ttgc 264

<210> 108
<211> 211
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-3-22 ; homology with orf 03 A.
thaliana

<400> 108
cttccatcaa gcagggactg gttgggggac tttatggtgt ggaaaccagc agttggtatg 60
gagaatagcc aatcattctg ggcaatttta acaatatgga tagctttggt tggagctgca 120
ctctttttgc aaaagtgaat catatacaag taaagctgtt tattgtctag ctttctattc 180
tttattggta tatatagtct gatgtgtatt g 211

<210> 109
<211> 262
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-3-3 ; homology with sequence 161 from
patent EP0953640

<400> 109
acattataat aggatgtaaa gaatgaagca ggaagcagtt tcttactaga acttctacta 60
taattgtgga tttatattgg gttgttcatt cagaaagctt tgccaagtaa cttagaatta 120
gtgtttacat tttgatgtct ttgttttgat attactaaga agaaaagata ttggggaaaa 180
aagaaagcca gaccactgaa tggcaggtct gatatgaaaa ctggccatgt atagaaggat 240
atttcgttta tttcattttt tg 262

<210> 110
<211> 265
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-3-4

<400> 110
gcttcaagtg gatgatgatg atattaaggc catgattaaa ttgggccgtg gtgatgaaaa 60
tggtggtggt gtcacctttg aaggtttctt ccaaattttg tctctttgat ttgttgcttt 120
gatgacgatg ataaatgtca gattaggtga acaagttttg gtttactttg tatttttcaa 180
tgatttgttt tactgtgctg cttcatatgc tattggctat tccgagaatt ctatttgaaa 240
acaaagaaga aaaagagttg ttccg 265

<210> 111
<211> 260
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g14-3-7

<400> 111
atgaagaaga agagggcggt ggtgatgact acattgagtt tgaggatgaa gacattgaca 60
aaatctaaat ctgaacgcaa agctgctgtt actgaggtcc gttataggcc tttctaatgt 120
ttttgtggag ctttttccat aaacattgag agtgtatctt gtgtatcgtt tgaagttatg 180
tatcaaactt tgtgcattgt gagttttgta ttagatttat gcttccatga aatgaatgca 240
atattctagc tggtgtctac 260

<210> 112
<211> 469
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g15-1-37 ; Arabidopsis genomic homology

<400> 112
atattcctgg aaacatctca acttgcatca tccccacttc gtcaagatct accgccaagt 60
gtcatactgc accatcttta ctcacgcggg cctgaagaac tacaatcacc attgcaaaga 120
aatagactta ctccgacgca gtattcactc tggatggatt cacaagggga ggaccaaatc 180
tggaaaggta ttaaagctac tctggacgac tatgctgcta aggtacggtc aagaggggac 240
aaggaattta gtcctgtcta tcctttgatg ctagaaatcg gctcttcttt atctgggaat 300
cgttagagga gctttgagag aatgcaaagc tcaaatcatc ttctcttggt atatgccctt 360
ccccatattt ttgtttcaat aatattgtca cagatgaaca catagcagac cgttatctat 420
gtttcgttta gtgtcttact ttctttatat attttacctc aattgattg 469

<210> 113
<211> 350
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g15-2-2 ;homology with ubiquitin [I] able
to induce HR-like lesions

<400> 113
gttgatgtcg ttgtgtcgtg ttgattgact gtgtctgttt ctggttgtgg tcgtgatgtg 60
ctttgtctac tgaggtctca aagatgttct atgctatttc tgtttgctgt ttctcttatg 120
ttctctgttg tgaataaaga ttccgaattc tgtcctaaaa aaaaaaaaat gaagtttatg 180
tatattggaa gaagcattgg tgtcgtcacc aagtcccatt tgatatatgg ctgtgttttt 240
gcttggctaa tttgtgttta aactttcttt ctatctgtgc tcaatatact cctgaacaga 300
ctgatgtacg attttaaagc tatgtatgta taaactctct tatcttttgc 350

<210> 114
<211> 345
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g15-3-11 ; homology with sequence 7 form
patent EP0953640 [I]

<400> 114
gtggatgaag ttaaggtgac ccctgttgct tagaagtaca cagagctttt gtaatggtca 60
atagagtttt ttgcaatgct aatttcatac ttattaagct accactgtga ggcaattgct 120
gtattttacc tatgtgattg ctttaaacta tgaattagat gcctgctgtg agacttgtgt 180
actattgctt ttaaggaagt gtggatctag ttgaacttcc tctcctttac tatgtgcact 240
ttgatcttga ttcttagata gtcaagaagt aatatataaa attgtactac tatatttcaa 300
atttttcatg tttcttgaag gatgaaatat aaatgagtta gtacc 345

<210> 115
<211> 344
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g15-3-7 ; Arabidopsis genomic homology

<400> 115
gatacatgga atgagttagt gtttgatctc atagggagag acttccagag tagacagagc 60
aatgcttcat aagaagaagg atccttaatg ctaaaaaaca tttttgtgc ttctacagca 120
cagctacggg aagattattt atctctctcg aatggagttt agcttttag ttactttaga 180
tctcttgttg tagctggtgt tgtaatctat gtttagatat ccacggtaag ataattccta 240
agttacacga aattttcaca ggtctcaagt atgtgtgcag ggatatttaa ctaaatacaa 300
acgttttctt tgcaataaaa tatttcatct gatttttccc tcgc 344

<210> 116
<211> 301
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g15-4-1

<400> 116
tgaatgttta atgttagaaa gtgaattact ctctttatgt ggtgtctgaa catatgttca 60
acattactct tcaaattacc aataattaat agtgcgacaa gttataggtt ataggttgat 120
gaaaaattgt ttccatcttg taaattatag tgctaaattt atcacacatc tgtgtgcacc 180
tatattatag tttctgcttt cattgaaaat gagtttcaag ttttctagtg gaattggata 240
tgtagtatag aagttggagg gttgcttttc attcttttga aagggtaaag caaacttaag 300
c 301

<210> 117
<211> 525
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g17-2-13 ; homology with wrky (zinc finger
DNA binding protein)

<400> 117
aagtggatat tttggatgat ggttatagat ggaggaaata cggacagaag gctgtcaaga 60
acaacagatt cccaagaagc tactaccgat gcacgcatca aggatgtaac gtgaagaaac 120
aagtacaaag gctgtcaaag gatgaaggag tagtagtaac tacttatgaa ggcatgcatt 180
cacatcccat tgagaagtcc acagataact ttgagcacat tttgactcag atgcaaatct 240
atgcttcctt ttgaaacgtc catcacttca atgcctaagg catgacactc aattagtcac 300
ttgtaaaata gtactacagt atattgtgta catgcgtttt gaacctagat gctatatttt 360
gaaataaaac gcaacttcat tagggaattt aatttgatca ttgtacaact aaaagtaatg 420
ttgctatttt tttgttttta tcactttgtt tttgccggag ccatgncttc attttaactc 480
tttcttttag aattaacaaa taattncatg ttggagaaga ncgtg 525

<210> 118
<211> 225
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g17-3-2

<400> 118
gaccaaatga gcaaattgaa gaaatgctgg agatcaccac atacttccag gcaaagcaac 60
ctcaattttt gttaccaaaa gatttcttga ttaaactttt gaaagtaaac acgtgtgtgt 120
agagaagtaa atgcaggcac tgggatttca atatcgtttc attgatgctg gtacagtagg 180
agattgaaac taaacatttt cttgaagttc agtacgtgtt cattg 225

<210> 119
<211> 412
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-4-7 ; homology with L18 (60S)
ribosomal protein

<400> 119
attgagaagg ctggaggaga atgcttgacc tttgatcagc ttgctcttag agcccctctc 60
gggcagaaca cggtactgct taggggtcca aagaactcgc gggaagctgt taaacacttt 120
ggtagagctc ctggtgtccc acacagccac acgaagcctt atgttcgggc aaagggaagg 180
aagtttgagc gagcaagagg gaaaagaaag agcagaggtt tcaaggtttg aggaattgcg 240
agtgtttgag tgcacgatga gagaatttct tttagaaggt tttccctacc tactttttac 300
catattagct tctttttctt gtcgaatttc ttatttcacc cctgtttctg tgacactcca 360
acctatagcc gattttgaat gcttttatta tctattctac gaaattaagc tg 412

<210> 120
<211> 373
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-5-1

<220>

<400> 120
acattatcaa gacgaaggca ataagtgggc ttactcattc ttactgaaaa acggggctgt 60
gaaatttgtt gtaatcttca agaatgtact tgttgccatc aatagaaaag caaacaatat 120
tgtgttcagt tacagccttg ttgggtcttg ctgagagtta tttttctagt tcctgaaagt 180
tatcttgcaa gctatcatgt agctgtgtgg taattttcac aggtttgagc tacagttgaa 240
gccagtaaca tgtgttgata ttatagctaa aataactaat gcttacctgc agtttccgtt 300
tgtgtggaat aaggagaaga attgatgtgt aagcatggct tctgtgagtt gactctatta 360
tctattgcat tac 373

<210> 121
<211> 390
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-5-12 ; homology with
capsanthin/capsorubin synthase, promoter region

<400> 121
ggttgcaagg gtgtatccga accctatttg cagaaaaatt atactgtata tacaaggtca 60
aaattatttt ttctgtttat atagttagat gttaaattgt cttggctttt tcgtgtattt 120
atttctttat attttgaatc ttcttggtga aaatcctagc tctgtacaca caaagagccg 180
acatgctgat ctctctctct ctctggacgg agagtcttct gaagtgattt tgtgcttctt 240
cagtgtgttt atagatcaat ttagtgtctt tgtcaaatgg atttctaagt gaaaaaagag 300
aaaaagtatt tcaatgcgtg tgacctacct tgcataaact ctgcatgatg gatatacaat 360
gtttctgctt gatatatgta tatgttttgg 390

<210> 122
<211> 381
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-6-12

<400> 122
tcttgcacga ggctggttat acaagggact catggttgct tctgaatgac ttcattaaga 60
tcctggacca ccctggtttg aagatggagg tagaagtacc aattgactag ttacacctgc 120
aatttcattt actataattc agatgtatct gtgtacaagg cagccgtgtt attctgtttt 180
gttgaattcg cgcacctgca ttctcctgct gtttttgtt aaatctcttt ctttttcctt 240
cttttgcccc cgttttatgt ctgtttgcgc ggcagggaca gaaacagaga aaccgccgtg 300
taattaagat aaaagctttc agcttattca gaagatcttg aatatgctat aattttaatc 360
tctcacaaac tgtgtatctt t 381

<210> 123
<211> 356
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-6-5

<400> 123
ttagagaaaa agagagagga aaatcgtaga aaaatcttca aaaaactgag ttgagtaaaa 60
tttcaaaaaa ttttagttgt catttctctt ctggtctttc ctttccagtc gatctcttct 120
tcagaaaaca aaaaaaaatg gttcaacttt agttttgagt ccagatttga tctcatttct 180
ttgctagagt ttcgtttgct gttatttgct ggtttttgc tttacccgtg gctgaacttc 240
cttcatcttt atttctgctc tctaccagct atttcgagct ttatttgtta agtattctag 300
gtacacactt tcaaatctgt actgtttctt catgaaaagg gctgaaaatt ttgaat 356

<210> 124
<211> 293
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-7-5 ; Arabidopsis genomic homology

<400> 124
aagaaaagta gcaccagggg cttgtccttg ttgtggagga aaagtacaag ctgtagatgt 60
agaaggccgt ttcagatttt gctttctccc tatttgcttt aggttcaaga ggaagtatct 120
ctgtactctc tgttctaagc gtttggtttt gtattcttga tctccctatt ttcctcttgt 180
aatttctact ctcaattttt tgaacagcat cctataagtg taattattta tttgaaatag 240
tgtttgagag ttgttcattt gctcaagaat atatgaaact tttgtagttg tgc 293

<210> 125
<211> 259
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g18-8-7

<400> 125
tgaagatgta gataaattgc tggaagatat aggggatgat gttggtgctg atgatggtga 60
cgatgaaaac tagaatgatg ttttttttct caagtaaatt tatntcattg tatttcttgt 120
tagtttttct cttctccact cccctctgtt tttctgtggc gcataggttg tacattgtaa 180
aaatttccca ataccaacat aatttaagga tgtaaaccat cttcttgctt tgcttgtaat 240
ttctctacta ggttgcttt 259

<210> 126
<211> 491
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g19-1-5 ; Arabidopsis genomic homology

<400> 126
ggttttaata agcttattgg tggttggttg ttcgagtttt ttggttactt taggagaggc 60
aagtggtagg tggacgagtt ttggggttat atttcaaatg gtagtgagtt caggatttgc 120
aactctgtta atgcttcaga gtcttgctgt gaacgtggtg ttgtatatgt attgcaaggc 180
atatcgtggg gagctggcgt ttgagatcgc ggaggagttt gcgagtcagt atgtgtgttt 240
gccttttgat aatgagaagg ttcctcatct tgtttgtgtt gttcaagatt gaatgtgcct 300
aaggtcagtg agattatgtt aggatgatgc agttagtagt ttgaagaagt agtgttttgt 360
tttactcgta gcatgtatat agtttcttgt ttgttagata aatgattgaa gatgtgtgtt 420
acctgttggc aatgtgcatc tttatatgta aaaaaagctt aatacctgtt atgaaattcc 480
ctccnagttt t 491

<210> 127
<211> 485
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g19-1-6

<400> 127
taggaaatga cctttgcagg agttaaatca tataaatatt tttttggact gcaaataatg 60
ataattttc tttttctaac caaagcaaaa taatatcatt tgtgaaattc agtcggtgta 120
cctgaacatt attagtatta aaatggagaa atgagagaac acgtatggcc actagagata 180
ttaaagctac ctaaatatga caatagatga agcagaggac agtataatat aattttcttt 240
taactataac atacattgcc ccctttatag atcaaagttt ttctactatt atttaattta 300
ttactataat aatcatctct ctctaggcgg ctagttggga ctatgctcaa cttgcaatat 360
ttaattttgt tttcatgttg ttcctttttc tggatgatgt tttaactgtc gaaaaaattg 420

agagctaagt tgcatggttc tgagttcgaa ggattaaaag caatgtnaat caattggctc 480
tatgc 485

<210> 128
<211> 484
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g19-1-7 ; Arabidopsis genomic homology

<400> 128
ggaggaaaga tctaggaatt tttccgagtt tgaacaattc ttggttgatc gtttctaccg 60
tcaatgaagg cagaaacagc ggttttgaat ccacctctca tctcttttga caacaagagg 120
gatgcttatg gatttgctgt acgacctcag catgtacaaa gataccgtga atatgctaat 180
atctacaagg aagaagagga agagaggtct gataggtgga acgatttttt ggagcgtcaa 240
gcagagtctg ctcagttacc cataaatggg atatctgcag acaaaagttc tactaatcct 300
ggtgccaaac catttagtca ggaggtaagt tgtgatgcac agaacgggga agaaggtcaa 360
cttgaaaatg caactgagaa ggatgtcata ctgacctctg tggagaggaa aatttgtcag 420
actcagatgt ggacggaaat tagaccctct ctacaggcag ttgaggatat gatgaacact 480
cgtg 484

<210> 129
<211> 224
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g19-2-1

<400> 129
tttttttttt ttgggtggcg gaggaaagcg tgtggaaaaa aagaaagaaa aaagagaacc 60
atagagttaa aggccagatc atgtctgcta tgagtcatca tctgttgttg gaagagaatt 120
cacttgttta attttacttc tcatatttta tatcatggga tttcatgttg gatggatgga 180
ccagtgtgta tgtcaaatta attcttattg cgaaaaaaaa aaaa 224

<210> 130
<211> 198
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g19-2-9

<400> 130

ccagtgtaat tggactttgc gcaattgaga gacaaggggt tagaggtata tacgtgattg 60
aagatcgtga tctatcttgt tatctctcat ttttttgaga tttttctctt cttcttttc 120
cccaaatctg taattgatga gattctagac agtgttagtg tataatcact agataatcta 180
tgtataatca gtttatcc 198

<210> 131
<211> 204
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g2-1-2 ; homology with 5-epi-aristolochene
synthase (sesquiterpene cyclase) [I]

<400> 131
ggactccatc gaagtttgag ctgccaattg ttgctcatct taaagaaact tcattcttct 60
gtgttgagaa agtagttata tatgtttttt taaattgtat aattaagttg ttaggaagct 120
ggttttgcga ttgtgcagtg gacttcctaa ctaggacctc cttgtaagaa gtaatcttca 180
agtgttatga attcacttgc attg 204

<210> 132
<211> 313
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g20-2-20 ; Arabidopsis genomic homology

<400> 132
tgcgagaaag accaagaaat ttgtattaga gcaaaaaatg gtgcttgggt gatttcgcgg 60
gtgacacgag ggaaggagct ctatatggta cttgagaaag ccaatgagac ccttctttat 120
gcctctgaag ctgttgaaaa gttcagtgac aggtattgca gtggcgcttt ttctttgtaa 180
gagggaaact agatttggt attgccgaga cacaggattc atacaaaaga catagctaca 240
tatcttatgt tgttgttaat tcaactttgt ttgtactgtt tataaataaa taaaaacttg 300
atcctctcct ctt 313

<210> 133
<211> 315
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g20-2-29

<400> 133

ttgcaatgaa ctttgtaact aaggtgggct ataaagaagg tttgggaact tcttatattt 60
agttgtttac gagacaaatt cgtgctttcc tggtttatca agaaaagaat tggtcaactt 120
aatgaagcat gtctccacac tgatctatct attctgattt ccagtgtaac agcttttttg 180
gccattacag tggttatttg atgatcacta gcattatcat atctagtaaa gtaaacacgt 240
caagtcaatt gatccattca actgtaacta tgctgaattt tacttatgga aaattcggaa 300
aatactattt acttc 315

<210> 134
<211> 315
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g20-2-31

<400> 134
agaatatagc tactacaagg tggttctccc agtagatcaa ctcaaagcca ttactccgtc 60
aactatgctg tcaagaattt gcaaggtgca ttgctgggtc atcattcgta gctagcgtgt 120
cattttcttg gtcatttcag atgaggtccg tgacactggt gcttgctttt gttgtagata 180
aaattctgta aagtatgcac atctgggtga ttgattgttg catacatgct aatttatcag 240
cggtttggta tcttgtgtac atctgtttcc tgaatttttt attatctttt agtattactt 300
tggttggttc gattg 315

<210> 135
<211> 483
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g3-1-1 ; Arabidopsis genomic homology

<400> 135
attttgagac cagaagggaa gctcattgtc cgtgacaaag tggaagctgt aaccgaatta 60
gaaagcatgt tcaagtctat gcattatgaa atccgtatga cctattcaaa ggacaaggaa 120
ggattgttgt gtgtgcagaa aacaatgtgg cgaccaacgg aggttgagac actaactaat 180
gcccttgctt agctgcttag cgtgtgtgcg gatgctggtt gtatatcatt cgagaggctt 240
tcatgccacg gtgactagat agtttttcga ttaaattctt gttactgtat tcttgtcagg 300
ctaccgtgta ccattccata gcaaaattag tgctattatc actatatatt tgtggaaagt 360
aagttttgta atattatgtc attagttgtg gaggaggtgg acattcttgg aattgtaaat 420
gccattggtt taggacggtg gtaaaaattc aaaaacacca gaatgaaatt cgttttcaga 480
gcg 483

<210> 136
<211> 553
<212> DNA

<213> Nicotiana tabacum

<220>
<223> plasmid g3-1-4 ; homology with ADP-ribosylation
factor

<400> 136
atagcaatga cagagaccgt gttgtggagg caagagatga attgcacagg atgttgaacg 60
aggatgagct tcgggatgct gtgctgcttg tgtttgctaa caaacaagat cttcctaatg 120
caatgaatgc tgctgaaata actgataagc ttggactcca ctctctcagg cagcgtcact 180
ggtacatcca gagcacttgt gcaacttctg gagagggact ttatgagggg cttgattggc 240
tttctaacaa tattgctaac aaggcctaaa ccaacgtaga gttgttgcgg gttgatcctg 300
gatgcaggcg ggtttttatc tagttctttt tcctttttt cccgaacatt cccagaatct 360
gtgtggttat gaatatccct tgaaagtgat ttgcttcttg gtaggaccta ttgaaatgtt 420
tttgtaatac agtggttgga tatatgtaat tgtttgttta gtttaaagta taatgctata 480
atttgtaaca gagattagat gtttgatgtt tcattggtaa atggtaatgg tatacttccc 540
tgtttgttcc ttc 553

<210> 137
<211> 501
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g6-2-13 ; homology with ACC oxidase

<400> 137
gagctctggt aattaacatt ggcgatgctc ttcaaataat gagcaatgga cgatacaaga 60
gtattgagca tcgagttatg gctaatggca gtaataatag gatttctgtg ccaatttttg 120
tgaaccctaa gcctagtgat gtaattggtc ctttggcaga agtgctagag aatggagagg 180
aaccaattta caaacaagtt ctttactcag attatgtcaa gcatttcttt aggaaagctc 240
atgatgggaa agacactgtt gattttgcta aaatcaagta gaaattagtg gatctgctcg 300
aagaataaga agtgcgctta tattaagcta atgtattttt ctttcatgta tttttagtta 360
cgactactca gcaatttaaa aaaaaagaag agatagtctc atactgcaaa gtataggaga 420
atatttttgg gattaattag gtgttcgaat tttgtaccgg ataaattata attgagctgc 480
tgatattatg gcaaatttag c 501

<210> 138
<211> 373
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g6-3-7 ; homology with ATP citrate lyase

<400> 138

aaatagtaga gatcggttac ctgaatggtc tgtttgtgct ggcacgttct attggtctta 60
tcgggcacac atttgatcag aagagattga agcagcctct ataccgtcac ccatgggaag 120
atgttctcta caccaagtga agacgctccc aatagcagca cgcagaaagt cgcctgcttc 180
ctatccagca ttttatcgaa aagtgtttgt ttagtcattt gttgtgatca ttcttcttgt 240
tttctgctag tattttgtac tcctaagaac ttgctaagca tttctgtaag ttgttataag 300
agacaactct tttagtttca caccaagagt ttccttcaat tcctatatat caaagaaata 360
acacattcat tgt 373

<210> 139
<211> 301
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g6-4-4

<400> 139
gttgggggaa aaggcaaaaa gatgaagaaa aaggcaatgg aatggaagga attgactgaa 60
gcatctgcta aagaacattc agggtcatct tatgtgaaca ttgagaaggt ggtcaatgat 120
attcttcttt cgtccaaaca ttaagttaaa taagttacta catcatttaa tcttccttaa 180
atttcattct tgtgttcttg taagtctttt tcatacttat ttcccttctt actttcgttt 240
tgcattgtca cagtgtaagg ttggaagcaa ataatatatc ctgcttaatg tcgtttggtc 300
g 301

<210> 140
<211> 299
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g6-4-5

<400> 140
aggttataga tgaaagacca atggctttag taactgatgc tgttgcgaat gaagccaaag 60
ataaaggctc aagctagaaa ttgcagtaat actgatttta ttgctgtctt ctttaacatt 120
accatcacta actagttctc catttttctt actggtgtat ttactttcaa gtattttatt 180
tgatgaggcg atatctcatt acttttgttt ttccagttgt ttgctttagt gaatttatat 240
gctggaagga tttgaggtat tagatagaaa gcatcttctg atttaacttc aattatgtg 299

<210> 141
<211> 356
<212> DNA
<213> Nicotiana tabacum

<220>

<223> plasmid g7-1-1 ; homology with a A. thaliana gene
homologous to MEI2 (meiotic regulator)

<400> 141
cagtggagga ctcgaaatgg aacctgatga tcaaaataat ttgcttaatg gtattgcaaa 60
cttaagcatg tcttatagtt atccaaatgg tgctgcaact gttgtcgggg aacacccata 120
tggagagcat ccgtcaagga cattattcgt tcgaaatatt aacagcaacg tagaggactc 180
agagttgaaa tcgctctttg aagtagtgct taacttacca gtttctttaa atttgcctct 240
gttaattagc tatccttttt cgtacttcct ttattgcagt tgaaatgctt gtttctcatt 300
ttgtttgtgc aagagatatt ttcttttgga cgacttcata tgcttgaaca ttgttc 356

<210> 142
<211> 350
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g7-1-4

<400> 142
gctggtgatc aaggctttgg agatatcaaa gataaaatta tgataatgaa tttcaagaat 60
tccaatggcc agaatttgtc aaagaattca gatttatgga atttggaaga gtgaagaaga 120
gggaaagatt ggaaaacatc tttattgatc acttctgcaa acaacaacga gtagaggctg 180
atttagaatt taaagtttaa gagtttttat aaatttagag ttaaatattt gtatatattt 240
aatgaattgt ttaatatata tacaatatcg tcaataggtt attatacaaa tgataagttt 300
ttgtagggag tgtaaaggaa aaagttttga aaaagaggag gatttgtttc 350

<210> 143
<211> 481
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-2-2 ; homology with P glycoprotein-MDRP
(ATP binding cassette protein)

<400> 143
gcgagggcca tagtgaaaaa tccgaaaatc ctactattgg atgaggcgac gagcgcattg 60
gatgcagaat cagagagatt agttcaagat gcacttgacc gggtgatggt aaatcgtaca 120
accgtggtgg tagcacatag attatcaacc attaaaggag cagatgtaat tgctgtagtc 180
aaaaatggag tgatcgtgga gaaagggaag catgagactc ttatcaacat caaagatggt 240
ttttatgcct ctttggtggc cctccacacg cgtgcttctt agttctactt ttttttcatt 300
aagtaaattg tattcatttt aatttcgtta tctttttgac ttttgctgaa gaagagtttc 360
tttaatagtg tactgcaact catataaagc atagtatagt agcattcttc aattaccaaa 420
tgagagaagc aagtaaactt gcctccccga cttgacttga tgtgttctgg ttattaagtt 480
c 481

<210> 144
<211> 480
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-2-6

<400> 144
agcaggacta gtcaagttgc atcttcacat tagaaatgct tgtatatatg tgtatcagcc 60
tatcaggtag atgtgctaga aagtttttag gagcagatac aaccctggaa acctgtacag 120
cttcttacgt ccctttata cctgtactat aagtaggtag gtggtggcct gaaatcccat 180
aagccaaaaa aaatatacaa gtaagcttca ccatgctcca ttacttagaa actgtacagc 240
ttgtgattta ccaaatatgt ctacattagt cctaatattt ccttagatat acgtagccta 300
agtattaagt caaacctgag tttttcgaag ggaaactttt tgtagcaatt cccttgatgt 360
tgttgactaa cttctcagca gttgcaagtg aatttcattt attgtttgct attttcctgc 420
tgcgtatgtt ctctcttaaa attgtaaaat gtttctgttt gtttcacacc agcttcatcc 480

<210> 145
<211> 447
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-3-17

<400> 145
tggggacagc aaaacctcct tggttgtgcc agtgcaaaga ttcaagtgta acattaaaca 60
gggaacatgc tcagggaaag ctgaagatcg tagatgtctg aagttagttt tcccacgttt 120
tcactatttt agcagagatc cagaaggaag aggaggaaaa gcgttctacc ttaagcagct 180
agtcgtgttg tatcgtgcat atttcatttc tggtttggtt ttagatactt ctatgtacat 240
aaactatcaa ggtatttata tatgttcata ttttggcttt agctttcatt tcatatgcac 300
attcggctgt gggtctcctc tgtaaaataa tgagttctat atcattataa gcattaagct 360
tctcttgtaa ttgtatcagt aatattaatc tcttcatttc attagttcca tgactcaacc 420
atcagcagtt aataaagagt ttgtttc 447

<210> 146
<211> 450
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-3-4

<400> 146
cagtgatagc aaatcaagta attttgaagg ggcagctgat ggttctcaca atgttggtca 60
gagatacaga gagaggggtc agggtcagtc aaagcgtgga ggtgggaatt tccatggtag 120
gcaaggtggc tctggccgaa taaatgccaa ttatgattga ttgatgagga ggctaaaatg 180
tggatttagg tctttttagt ttgtgatgga tagcaaactt accggataat ctttgcttag 240
tctgcatgtc tggtggtgca gtcttaggtg gtagcttttg acgtggtaaa agagaatttg 300
ttggccaatg tcacacgggt gagctggact acagccgggt tttgccacat ggttttggga 360
aaaattattg tgtttggtgc aacagtaagt gcggcattat gagaactgta attaatttga 420
agaacattaa aatagttgcc cattttctcc 450

<210> 147
<211> 335
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-5-5

<400> 147
ggaaacacag aggcagagat gatggtgacg aggagattga cagatacttg ggagttaaga 60
acgggaaact atcagggaag ctatcaaaga agccaaagag aaaatgagga atatataatt 120
aagctatttt agtccaattt tgacttaatt gaggaatatt ataattaagc tatgttagtt 180
caattttgaa cttaattagt tctttcatta ttccttgttg ggctgtaatt tgacatttct 240
gcaattctgc tgggatggtt ttgatcttag ggactctatt attttcattt tcttgtgaag 300
atccttgcct cctaatccta atatatacgt gcacc 335

<210> 148
<211> 245
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid g9-6-1 ; homology with LOX lipoxygenase

<400> 148
gtgaaagtgg acttactgga aaaggaattc ccaatagtgt ctcaatttga ggttctacag 60
cacgaatagc tgatatatag cttttgcagt cctcgtcaac ctgcagaaat catccgcaac 120
ttaagcagga gtggcaacag atgtgtgtag atctattttt atgtcaatat ttgtttagcc 180
aaattccatt attgttagtg tgtgttttta caataaaatc aatgagcaaa tcccctcatt 240
ttccc 245

<210> 149
<211> 353
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t12-1-7

<400> 149
gcattgcggt gcctatccaa agatcctcgg tttagatcaa gcatgagtga cattgttaaa 60
gaactagagc aactttatca acaatctaaa gatgcaggta atactcgcag ccacggtaac 120
aaccggccta gaccacgtag ncgaagtgct ggtgatgttg gtaataaaca tacttcagtt 180
gcttatccaa gaccgtctgc ttctcccctt tatgctaaat aattcaataa atgatatgat 240
gccttttcat gttttgcctt tatgtttttc aagctgaaga acctgcacat ttgcagaatc 300
agctgattgt acagttgttt tggttaatgt attggatgtg tttgtaacct tga 353

<210> 150
<211> 351
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t12-2-1 ; homology with chitinase class 4

<400> 150
gtaatataat cgtatattct ttttaaaata naatcatgta tagtggagtc tnatgcaatt 60
ctcanaacat atatatgtcg ncctcactac cgggggagca actaatantg aatatctnng 120
gttatncttt gattcaactn ctggnnatna cttacgtcct aacatgtnag attatcccca 180
gtctccagac ccagtngttg acganactca gtataatact cagcccttcn ggcaacagtc 240
tgaaggtgga nctccgncac atncnatctg gccattaatg gctcaaatgg ttgggccaag 300
accttgggna naagntgatg aaagaatggg ngnttggtnc gnncgatanc a 351

<210> 151
<211> 352
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t12-2-18

<400> 151
gaatagttga acttattttt caaatggcan aaatggactg acttaacttc tgtacatnag 60
ctataaagat gataatcaga gtgcctnctg catntcatcc tcttcttgga antgcaagaa 120
ctggaagccc ttcattgatg tggagtgtaa acgtggtnct ataagttant tctttcgtgt 180
cgtctgatag tttgaacctg anganatgaa gaagagctan tggnnaagat ctncatgngt 240
caataaanga gatcttngcc taaacanatt cgnggacnag cgtgaaatgn tagggaatgt 300
gaatggtaac gctggnctgg aagaagancc nntccngnca agncaanctt tc 352

<210> 152

<211> 424
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t18-2-5 ; homology with basic PRB-1b [I]

<400> 152
gttcgatgca acaatgggtg gtattttata acatgcaatt atgatccacc tggtaattgg 60
agaggacaac gtcctacggt gatcttgaag agcaacatcc ctttgattcc aagttggaac 120
ttccaactga tgtctagtaa taacggttta cgtgatcaaa taatgaataa aagctttgtc 180
atgtgttaag gaaaattaaa taaataccag tactatgcta tgtgatgtta tcttcttacc 240
cagtggataa taatccaatg gtgtagcaag gggtggattt actgttatct acttgtttta 300
catttgtttt tggtggtatt atggaggtgt gtatatgtat gtgttttgat gaataaacaa 360
agtgaacaag gtgatgagtc aacagcgatg taaatttgtt ctttgattaa tataattact 420
tact 424

<210> 153
<211> 277
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t18-3-2

<400> 153
ttcaaagttt tcgttgccct accaaccacc ggtggatgtn gctcctccng cccacaagtn 60
aacctgatat cttnttgttt tcctntagta ctagaaaaat ataangtagt attagttttn 120
cattctttca atgtgtgcag ttacatccct atcttttggg aggatacatc atcctcgnca 180
tcattggact tgaagtacca ccttaatcng taaccacaat ttttnaactt taaataatat 240
caaatttata atgacaaata tgttncttct ccacttc 277

<210> 154
<211> 366
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t18-3-6 ; homology with chloroplast RNA
binding protein

<400> 154
gtactatatg atggtgagac tgggagatct cgtggctatg gtntttgtga gctatgagaa 60
tagagaacaa ttggagaatg cccttcaaaa tcttaatgga gtggaactgg atggaagggc 120
aatgcgcatt agcttagcac aagggaagaa acaataagat ggacaagatt cttgtatatt 180
agttgtaaaa gttgaaaatt taccatcaat agaagaacaa tgttttattc atggattaag 240

atggctaaag gcttttaact aggacaaagg gagatgtacc atttgaatta catcttccat 300
aggttgagct ttctatcttt gtttctttac tgcctttcat aatttagaga tatcattgtt 360
cctttc 366

<210> 155
<211> 282
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t18-4-18 ; homology with AGP-b (ADP-G
pyrophosphorylase, small sub.)

<400> 155
gtaatcaccg gtttttattt taaacgaata atttttacag tacctantct nctcttgtag 60
gggtaatgag aantatctag ctacataaaa gtnggatgtg cgctanattt ctacaggnaa 120
agcaaaatna aagtagaana tttctaccgc atggctgttn acccaagatt tgggaggaca 180
accaagtncc aangcctncc ttcanatgat aatgccactg ggaatcaatg ngtccttgat 240
nacngtgana atcccnctct agannaagta tccatctgtt tc 282

<210> 156
<211> 376
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t2-1-1 ; homology with ubiquitin
conjugating enzyme

<400> 156
accagaaatt gctcacatgt acaagaccga caggtccaaa tacgagacca ctgctcgtag 60
ctggactcag aaatatgcta tgggataatg gcaaaggcgt caccaggcat gtctgagact 120
ttgtaacagc aatgtcttat tgtgctggtg gtgaatgaat aaattcggcg aaagaactta 180
gtttacttct taatctccct taaagtgggt tgtcaagaga catgtctttt caatttgtga 240
atatctattt gatgactatt agtaagggag aaacttcatg taattttact ttgtttgcca 300
gtttacctga gcctttctct agtttttcca atttgcctgg cttgtttggt tctgcgttca 360
aagttggtat tgattc 376

<210> 157
<211> 364
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t2-1-3 ; chloroplast genome [I] homology

<400> 157
ggnnnncaat ngnnatcgna cnagnnnncn gnannannan tccaaagctn tcnaatnttc 60
tccattactt gtgtggataa gcccnatatn atagagtata taacttcgat catagggatc 120
aatttctagt cgcatagctt cataataatt ctgcaaagct tccgcgctaa tttccttcgg 180
atctgagccg acatcccatc tctgtaatag gtaaatgcct ctttttctcc tgaagttgtc 240
ggaattactc gtaatangat attggctaca attgaaaagg tcttatcaat aaaatttcca 300
tttatccgtg atctaggcat aggtagcaat ccattctaga attcttctca ttacctctca 360
tggg 364

<210> 158
<211> 184
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t2-6-3

<400> 158
gagatcagta tacatgaaat ggtatatacg aggacatagt ttcctttagg gaaatgtcaa 60
taggttagag aagaatggtt aaaccgccgg cccgacggtt taattaggtt attatataat 120
taggtttatc ttttgacttg tatgttatta gctagtaata atatacttat tcaattttgt 180
gccc 184

<210> 159
<211> 534
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-1-12 ; homology with SNF-1like kinase,
calcineurin B-like calcium sensors interacting
protein in Arabidopsis

<400> 159
ccagattaag cttcaggggg agaagaccgg gcgcaaaggt catttatccg ttgcaaccga 60
gatttacgag gtggcacctt cactatacat ggttgcttcg caaggctgga ggagatacct 120
tggaatttca caagttttac aagaacctgt ctaccggatt gaaagacatt gtttggcaac 180
tgggggaagg aggagaggaa gtaaaagatg gtcttgtcgc agcttgattt tggagtgtga 240
agtcagtggt ttgccaatgt gaataactct gcaaacagtg tgctagatat tagataatgc 300
tgtgctgtaa aaagaacttt ttataatcag ttgatgtcaa acagagtgtt taagcatcaa 360
cgagtttata atacattgtt ttatgtacga ttaaggcacg taaacttaga aaaattaaga 420
ctggttttac attgccattg ttgtcttatt tggtgacaag atattacgga tcaatacccc 480
ccccaaaata tgtgctttta ttgaactgga agtggtaaca aagtgtgtta tata 534

<210> 160
<211> 398
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-2-4 ; homology with a multi-functional
protein -beta oxidation

<400> 160
cctcagaaac gcaatggagg tgtcatgttt tggggntgat acaattggat ctgaatacat 60
atactcaaag ctaaaaactt ggcatgaggc ctatggtgat ttttataagc catcaacatt 120
tttggagcag agagctgcaa aaggattgcc cttgggagga tcgtgttgag ctgcatatca 180
tatgatcata tccttgcaga agaagcagta attcaagcat gctgaacttg tgntcggaaa 240
taaggcgggn aagtttgtta attacaatta gttagnagtt ccattaatta taataatttc 300
ctatttttc ccctcaagtt atttgatggt agttgtaact ttggctctac aaantagtgt 360
aatcgtccga gaaagagaat gaaatgtcca aacgcttc 398

<210> 161
<211> 398
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-4-7 ; homology with GST (bronze-2
protein homologue)

<400> 161
atggggttgc tagatatcat gatcattatt acactagggg catacaaagc acaagagcta 60
gtgtttggtg tgaaaatatt ggatgcagag aagacacccc tcttatactc atggttgact 120
agtttaattg agctgcctat agttaaggaa atcactcccc cttatgacaa ggtgctttca 180
tttcttcatc ttctcaaaga catcgtcttc aaagctccgg ccaattgacc tttttgtgt 240
ttatgtccat ctctgtctct tttgtctact ccactcatta attgtactca atgtcttctc 300
ctctgtattg tataatataa taaggcttat ggccatttgg attccaaagg ctacttatat 360
tttgagtgtg tgttttatac aacagaaagt tatcatcc 398

<210> 162
<211> 397
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-4-8

<400> 162
ccatgagaat gacgaaagca aggcagaaaa gaaaggagaa catgataaga agaatttgat 60

gaagaaggtt gctgggaaaa tagggaaaaa attattgcat agtcatccta agaagcagca 120
tgaggaaggc tatgaaggag aagaggagga agaaggagaa gaaggagaag aagtagaagg 180
agaagaagta gaagtagaag aagcggnaga aggtggtttt gaatttgaac tcnactttga 240
tttttgatta agctttatgt atcactccag ctgtgtacgt tggtatttct ccttattggt 300
ttaaaaanac ataagtatgt ttcgaggata tctctgaata ggtggcttgg natttgtaac 360
ctgtggtacc atatatatga gcgtcttcta gtttttt 397

<210> 163
<211> 304
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-5-4

<400> 163
acgaatgtgt ttagtactcg gggcaactcc aagtcttgag atccaagtgt tgcagcctct 60
ttagccttta aaaggtggat gctgccattt taacctggtt ttagtttgga tgaaatttga 120
attcaaagct tttgtttgta gcttaggttc ctgtattagt tttcagttga aatagttgtg 180
tactctttca tctttgagca atgaaataaa agtcctcaaa tctgcttctt ttagaactaa 240
aaaagatctc ttatattttc ccctgtaaaa tcttgcaatt gattatcaac cgtcctctct 300
tatt 304

<210> 164
<211> 307
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-5-5 ; Arabidopsis genomic homology

<400> 164
gagctgataa atggaaaagc agcagtaatt ggtttcctat tgctgttgga ttttgaactc 60
ttgaccggta aaggtcttct caaaggaaca gggttcttgg atttcattta ctcagtttca 120
gatgctttca aataaaacca ttccgctata tacttactcc ccctccctct ttttcccctt 180
ttcctatttt tctgacaaat ttgcatttgt ttaaataaac aaaaacaaag aatgttgatc 240
tttttatatg ttgtccaatt atatggatta gtgaattata gaccattgaa ttccagctga 300
agaatgt 307

<210> 165
<211> 192
<212> DNA
<213> Nicotiana tabacum

<220>

<223> plasmid t7-6-4

<400> 165
aacaataatt ggctataaca ttcaaaaata tttgaaacaa gcgatgccgt tacgtagagg 60
ttttacggta aaagtagaag ctggtataag ccatcaatgg aaaaactgga taattcgatc 120
ttatataaat ttcctaatgt attgagacta atatatacag tcggatttta aggttttggc 180
cgaccggatt ac 192

<210> 166
<211> 232
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid a1-1-17

<400> 166
agagaaagat ctgtacgtaa ttgccaaaaa cgatgagtgt ttggatgtca tgctttattt 60
tggtgtttat nggtgtctcc cttttgtatt tgaagttttc ccagaaaatt agcaaagaat 120
aagcttcaaa ctggttttac attttnggtt caaaatgtca natcaaanaa tctgtnatgc 180
tattggtgtt gtatgtaata attagatccc attttcttcc tctttccttt at 232

<210> 167
<211> 489
<212> DNA
<213> Nicotiana tabacum

<220>
<223> plasmid t7-1-14

<400> 167
ccctcagaac gcaagtagca acagtttctt caattgctat tgcctatctc tgaactcgaa 60
ttcattactt gtaagatctg ctaataatca ctatgttttt ctgcagtgga ggtgtcatgt 120
tttgggctga tacaattgga tctgaataca tatactcaaa gctaaaaact tggcatgagg 180
cctatggtga tttctataag ccatcaacat ttttggagca gagagctgca aaaggattgc 240
ccttgggagg atcgtgttga gctgcatatc atatgatcat atccttgcag aagaagcagt 300
aattcaagca tgctgaactt gtgctcggaa ataaggcggg aaagtttgtt aattacaatt 360
agttagaagt tccattaatt ataataattt cctatttttt cccctcaagt tatttgatgg 420
tagttgtaac tttggctcta caaactagtg taatcgtccg agaaagagaa tgaaatgtcc 480
aaacgcttc 489

<210> 168
<211> 877
<212> DNA
<213> Nicotiana tabacum

<220>
<221> CDS
<222> (31)..(588)

<400> 168
aacttcctct cttaaagttc atttactttg atg gag aat tat caa cat att ctt 54
Met Glu Asn Tyr Gln His Ile Leu
1 5

cca aat tac tct tct tca tcg tct gat cag ttg tca gta atg aat atg 102
Pro Asn Tyr Ser Ser Ser Ser Ser Asp Gln Leu Ser Val Met Asn Met
10 15 20

atg aac aac aat tct caa gca aaa aca act gaa tta acc caa gac aat 150
Met Asn Asn Asn Ser Gln Ala Lys Thr Thr Glu Leu Thr Gln Asp Asn
25 30 35 40

aag aaa tcg agc ggg ttt ttg ggg cta atg gca agc atg gaa gct cct 198
Lys Lys Ser Ser Gly Phe Leu Gly Leu Met Ala Ser Met Glu Ala Pro
45 50 55

agc tcc agt gtt gtt act gat cac cca aat agc att ccg tat aac cct 246
Ser Ser Ser Val Val Thr Asp His Pro Asn Ser Ile Pro Tyr Asn Pro
60 65 70

aat gat cag aac gag gtg aga tcg ggt aag aag aat aaa gtt gag aag 294
Asn Asp Gln Asn Glu Val Arg Ser Gly Lys Lys Asn Lys Val Glu Lys
75 80 85

aag att aaa aaa ccg aga tat gct ttt caa aca agg agt caa gtg gat 342
Lys Ile Lys Lys Pro Arg Tyr Ala Phe Gln Thr Arg Ser Gln Val Asp
90 95 100

att ttg gat gat ggt tat aga tgg agg aaa tac gga cag aag gct gtc 390
Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val
105 110 115 120

aag aac aac aga ttc cca aga agc tac tac cga tgc acg cat caa gga 438
Lys Asn Asn Arg Phe Pro Arg Ser Tyr Tyr Arg Cys Thr His Gln Gly
125 130 135

tgt aac gtg aag aaa caa gta caa agg ctg tca aag gat gaa gga gta 486
Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ser Lys Asp Glu Gly Val
140 145 150

gta gta act act tat gaa ggc atg cat tca cat ccc att gag aag tcc 534
Val Val Thr Thr Tyr Glu Gly Met His Ser His Pro Ile Glu Lys Ser

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        155                 160                 165

aca gat aac ttt gag cac att ttg act cag atg caa atc tat gct tcc    582
Thr Asp Asn Phe Glu His Ile Leu Thr Gln Met Gln Ile Tyr Ala Ser
    170                 175                 180

ttt tga aacgtccatc acttcaatgc ctaaggcatg acactcaatt agtcacttgt    638
Phe
185

aaaatagtac tacagtatat tgtgtacatg cgttttgaac ctagatgcta tattttgaaa 698

taaaacgcaa cttcattagg gaatttaatt tgatcattgt acaactaaaa gtaatgttgc 758

tatttttttg tttttatcac tttgtttttg ccggagccat gctcttcatt ttaactcttt 818

tcttttagaa ttaacaaata atttcatgtt ggagaaagat acgtgccaaa aaaaaaaaa  877


<210> 169
<211> 185
<212> PRT
<213> Nicotiana tabacum

<400> 169
Met Glu Asn Tyr Gln His Ile Leu Pro Asn Tyr Ser Ser Ser Ser Ser
  1               5                  10                  15
Asp Gln Leu Ser Val Met Asn Met Met Asn Asn Asn Ser Gln Ala Lys
             20                  25                  30
Thr Thr Glu Leu Thr Gln Asp Asn Lys Lys Ser Ser Gly Phe Leu Gly
         35                  40                  45
Leu Met Ala Ser Met Glu Ala Pro Ser Ser Ser Val Val Thr Asp His
     50                  55                  60
Pro Asn Ser Ile Pro Tyr Asn Pro Asn Asp Gln Asn Glu Val Arg Ser
 65                  70                  75                  80
Gly Lys Lys Asn Lys Val Glu Lys Lys Ile Lys Lys Pro Arg Tyr Ala
                 85                  90                  95
Phe Gln Thr Arg Ser Gln Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp
            100                 105                 110
Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Asn Arg Phe Pro Arg Ser
        115                 120                 125
Tyr Tyr Arg Cys Thr His Gln Gly Cys Asn Val Lys Lys Gln Val Gln
    130                 135                 140
Arg Leu Ser Lys Asp Glu Gly Val Val Val Thr Thr Tyr Glu Gly Met
145                 150                 155                 160
His Ser His Pro Ile Glu Lys Ser Thr Asp Asn Phe Glu His Ile Leu
                165                 170                 175
Thr Gln Met Gln Ile Tyr Ala Ser Phe
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180 185

<210> 170
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer EVVRA
26

<400> 170
cgcgcagact ctcgagggcc c 21

<210> 171
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer EVVRA
28

<400> 171
ctcagatcta gaagttcatt tactttgatg 30

<210> 172
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer EVVRA
29

<400> 172
attgaagatc tagacgtttc aactcgaggc 30

<210> 173
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer EVVRA 30

<400> 173

ccctcgagcc accgtactcg tcaat 25